Copyright

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Result
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Maximum DB
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                                                                                                                                                                                                                                                            Score
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   US-09-065-672-5
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  Q60667
Q30159
X30159
T18324
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V20441
V83940
V83939
T25057
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Q95493
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BRCA1 gene 5' tran
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Cdn-2 DNA. N
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Mutate	T17520	_	24029	6.1	21	
BRCA1,	T32612	1	24026	6.1	21	
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Mutate	T17529	_	24026	6.1	21	
Mutate	T17528	Н	24026	6.1	21	
Mutate	T17527	_	24026	6.1	21	
Mutated BRCAl geno	T17526	Н	24026	6.1	21	
Mutate	T17524	L	24026	6.1	21	
Mutate	T17523	Н	24026	6.1	21	
Mutate	T17522	_	24026	6.1	21	
Mutate	T17521	ш	24026	6.1	21	
Mutated	T17519	L	24026	6.1	21	

ALIGNMENTS

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RESULT 2
(Q95493)/c
ID Q95493 standard; DNA; 6511 BP.
AC Q95493;
DT 21-NOV-1995 (first entry)
DE Human Cdn-2 DNA.
KW Cdn-2; apoptosis modulator; adoptive immunotherapy; therapy; HIV;
KW autoimmune disease; reperfusion injury; hepatitis, osteoporosis;
KW autoimmune disease; ss.
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Eliman HCMV inducible gene, SEQ ID NO 21.

HCMV inducible gene; cig; human; human cytomegalovirus; interferon;

wanti-viral therapy; anti-HCMV therapy; detection; diagnosis;

Homo sapiens.

New Mo9913075-A2.

New
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated human genes
Claim 2: Page 143-147; 184pp; English.
This sequence represents a human gene of the invention, that is induced to express by both HCMV and interferon (IFN), designated HCMV-inducible genes (cig or cigs). The invention also relates to genes that are repressed in the presence of HCMV infection, designated HCMV-repressible genes (crg or crgs). The products can be used to obtain agents which can be used for anti-viral therapy, particularly anti-HCMV therapy. They can also be used for the development of drugs that would allow for higher dosage IFN treatments without the concomitant toxicity normally associated with administering high levels of IFN. The products can also be used for detection, diagnosis and drug screening.

Sequence 3200 BP; 972 A; 629 C; 742 G; 857 T;
                                                                                       Homo sapiens
Key
W09515084-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X33947;
30-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 380 CAGGAGTTCCAGACCAGCCTGGGCAA 405
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                                                   Location/Qualifiers 3312 .3947
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Pred. No.
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RESULT
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A single-stranded DNA (or its complementary strand or the corresp.

double-stranded DNA) which comprises one of the 7837 "GS" sequences

given in T19001-T26837 and which is able to hybridise to part of

thuman genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)

sequences were obtained from 3'-directed cDNA libraries prepared

from various human tissues; synthesis of cDNA was initiated from the

3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-

cuntranslated sequence is unique to a particular mRNA species, almost
all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library

is constructed so as to reflect accurately the relative abundance of

different mRNAs in the particular tissue from which it was derived.

The appearance frequency of a given GS in a cDNA library can be

determined (esp. using primers and probes derived from the GS

sequences) as a means of diagnosing abnormal cell function or for

recognising different cell types.

Sequence 84 BP; 33 A; 17 C; 15 G; 19 T;
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30-NOV-1994; U13930.
30-NOV-1993; US-150067.
07-OCT-1994; US-320157.
(LXRB-) LXR BIOTECHNOLOGY I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene signature;
human; cloning;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1393 CAGGAGTTCCAGACCAGCCTGGGC 1370
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Cdn-2 CDNA was isolated from a human placental genomic library using a 950 bp fragment of Cdn-1 CDNA. Expression of Cdn-2 in mouse progenitor B-cell FL5.12 cells decreased IL-3-induced apoptosis. The Cdn-2 protein displayed 97% amino acid identity
                                                                                                                                                                                                                                                                                                                         Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                       Claim 1; Page 1942; 2245pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                  WPI; 95-206931/27
                                                                                                                                                                                                                                                                                                                                                                                                    Matsubara K,
                                                                                                                                                                                                                                                                                                                                                                                                               11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human gene signature HUMGS08078.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-OCT-1996 (first entry)
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WPI; 95-215106/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         289 CAGGAGTTCCAGACCAGCCTGGGC 312
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                                                                                                                                                                                                                                                                                                                                                                                                  Okubo K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         messenger RNA; mRNA; relative abundance; frequency mapping; non-blased library; diagnosis; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequences encoding Cdn apoptosis modulators - and transformed cells, proteins and antibodies, useful treatment e.g. of HIV infection, reperfusion injury
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Pred. No.
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Query Match Best Local Similarity

6.6%; 100.0%;

Score 23; Pred. No.

DB 1; 0.0056;

Length 84;

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RESULT
V39298/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    cc acid sequence encoding human RAD54 (hRAD54). A method for analysing a specific growth of partial nucleus candle sequence of at least 15 and no more than 30 consecutive bases of the DNA sequence encoding hRAD54 has been developed using a DNA sequence encoding hRAD54 hrad54 is a gene thought to be present in tumours that display allelic imbalance at IP32, the chromosomal band cidentified as one of four minimal regions of chromosome 1 deletion in the present in the care of the DNAD54 is useful for production of proteils, inter alia, that have been identified as novel hRAD54 by homology between the amino acid sequence given in W62186 and known amino acid sequences such as yeast RAD54 protesins are used in the treatment of cancer, including xeroderma Pigmentosum and Bloom syndrome, Werner's syndromes and x-linked mental retardation with alpha-thalassaemia syndrome and breast cancer. hRAD54 polynucleotides are also useful for diagnosis of disease or susceptibility to disease, hRAD54 polynucleotides are also useful for detecting cuseful for diagnosis of disease or susceptibility to disease, hRAD54 polynucleotides are also which are proteins greunder useful for detecting complementary nucleotides are also useful for detecting cuseful in gene therapy.

Sequence 840 BP; 190 A; 200 C; 221 G; 229 T;
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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Homo sapiens.

W09602552-A1.

01-FEB-1996.

19-JUL-1995; U09145.

19-JUL-1994; US-276919.
                                                                                        Non-small cell lung cancer; NSCLC; tumour marker; carbonic anhydrase; diagnosis; therapy; promoter; fluorescent in situ hybridisation; ds.
                                                                                                                                                                                  T15455 standard; DNA; 1363
T15455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human hRAD54 DNA and polypeptide - and agonists, antibodies, antagonists, etc.
Claim 1; Page 28; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SMIK ) SWITHKLINE BEECHAM CORP.
(UVJE-) UUIV JEFFERSON THOMAS.
Croce CM, Fishel RA, Rasio D, RC
WPI: 98-274189/25.
                                                                                                                          23-ADR-1996 (first entry)
Lung cancer specific antigen HCAVIII promoter region genomic
Lung cancer specific antigen HCAVIII promoter region genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-MAY-1998.
10-NOV-1997; 308998.
13-NOV-1996; US-030676.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; RAD54; hRAD54; cancer; xeroderma pigmentosum; Bloom syndrome; Werner's syndrome; ATR-X; diagnosis; detection; SNF2 superfamily; X-linked mental retardation with alpha-thalassemia syndrome; tumour;
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EP-844305-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a specifically claimed partial nucleic
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Pred. No.
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0.02;
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                                                                                                                                              DNA
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27-APR-1990; JP-113146.
31-JUL-1990; JP-204438.
14-SEP-1990; JP-245256.
28-DEC-1990; JP-415801.
                                                                                                                                                                                                                               New mutein(s) of proteins - with fibroblast growth factor receptor activity, useful for treating multiple endocrine neoplasia, prostatic hypertrophy, used for diagnosis Example 3; Fig 8; 88pp; English.

A CDNA library prepared from human cancer cell line Kato III mRNA was screened with an oligonucleotide corresponding to amino acids 529-541 of chicken basic FGF receptor. Three positive clones were obtained. One was cloned into pUCl18/I19 to give pTB1228 (see Q14048). The complete FGF coding sequence was obtained by ligating the insert from TB1228 to the DNA sequence of the plasmid pTB1281 insert which encodes the carboxyl terminus of the FGF receptor from Squence 2310 mards.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  useful for diagnosis and treatment of non-small cell lung cancer Claim 53; Page 62-63; 87pp; English.

A genomic clone (T15455) was isolated that constitutes the putative promoter of the HCAVIII gene (see T15448), and probably contains transcription regulatory elements directly implicated in expression of HCAVIII, a cell surface antigen which is highly specific for non-small cell lung carcinoma and which has features in common with human carbonic anhydrases. The clone was obtd. by PCR amplification using a primer pair (T15456-57) based on the putative exon 6 of the HCAVIII gene. A DNA probe comprising the genomic clone plus flanking sequences was used for fluorescent in situ hybridisation. Sequence 1363 BP; 352 A; 382 C; 369 G; 260 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TAKE) TAKEDA CHEMICAL IND KI
Igarashi K, Senoo M, Watanabe
WPI; 91-353723/48.
P-PSDB; R15269.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clone pTB1283 encoding complete FGF receptor. Human; fibroblast growth factor; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q14851;
18-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q14851 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CYTO-) CYTOCLONAL PHARM INC. Bollon AP, Torczynski RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid encoding the lung cancer specific antigen HCAVIII
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                                                                             289 CAGGAGTTCCAGACCAGCCTGG
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                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                       2310 BP;
                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                       6.4%;
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Pred. No.
                                                                                                                                       Score 22;
Pred. No.
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                                                                                                                                       DB 1;
0.021;
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0.02;
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T67164/c
TD T67164 standard; cDNA; 10380
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914
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Best Local (
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A cDNA library prepared from human cancer cell line Kato III mRNA was screened with an oligonucleotide corresponding to amino acids 529-541 of chicken basic FGF receptor. Three positive clones were obtained. One was cloned into pUC118/119 to give pTB1229 (see 014849). The complete FGF coding sequence was obtained by ligating the insert from pTB1229 to the DNA sequence of the plasmid pTB1281 insert which encodes the carboxyl terminus of the FGF receptor from
                                                                                                                                                                             exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-DEC-1990; JP-415801.
(TAKE) TAKED CHEMICAL IND KK.
Igarashi K, Senoo M, Watanabe T;
WPI: 91-353723/48.
                                                                                                                                                                                                                                                                                                                                                          gene therapy
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                Human alpha-N-acetylglucosaminidase gene. Alpha-N-acetylglucosaminidase; mucopolysa
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Sequence 2676 BP;
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27-APR-1990; JP-113146.
31-JUL-1990; JP-204438.
14-SEP-1990; JP-245256.
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14-NOV-1991.
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Human; fibroblast growth factor;
                                                                                                                                                                                                                                                                                 exon
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                                                                                                                                                                                                                                                                                                                                                                             therapy;
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                                                                                                                                                                                                                                                                                                                                                                           enzyme replacement therapy; diagnosis;
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1373. .211.
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3203. .3386
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2263. .3055

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Pred. No.
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0.021;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; w18017.

Nucleic acid encoding mammalian alpha-N-acetylglucosaminidase used for the diagnosis and treatment of mucopolysaccharidosis type IIIB, also used in gene therapy Claim 8; Page 54-61; 79pp; English.

A genomic DNA molecule (T67164) includes 6 exons that code for human alpha-N-acetylglucosaminidase (W18017), an enzyme that can human alpha-N-acetylglucosaminidase (W18017).
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W09315196-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            patients suffering from mucopolysaccharidosis type IIIB. Administration is by oral, i.v., i.p., enzyme replacement therapy, gene therapy or other routes.

Sequence 10380 BP; 2210 A; 2953 C; 2851 G; 2366 T;
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23-NOV-1995; AU-006748.
(WOME-) WOMEN'S & CHILDREN'S HOSPITAL.
Anson DS, Blanch L, Hopwood JJ, Scowpi; 97-298114/27.
                                                                                                                                                                                                                                                                                                                                                                                      Clone of recombinant human kappa casein gene fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                Q46852;
26-JAN-1994 (first entry)
                                                                                              intron
                                                                                                                                                                                               intron
                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                  Casein; supplement; milk; pharmaceutical;
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3473. Eff
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                                                                                                                                                                                                                                                                                             .8834
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Pred. No.
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0.022;
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AC DT

T71696 standard; DNA; 26764 T71696;

20-AUG-1997 (first entry)

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RESULT
T71696
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T71699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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25-JAN-1993;
23-JAN-1992;
                                                                                                                                                                                                           The present sequence encodes the human deoxycytidylate (dCMP) deaminase intron 2, which comprises 20303 base pairs from nucleotides 1964-22266 of the dCMP deaminase sense strand. The dCMP deaminase gene contains a 5' untranslated region (including the promoter), 5 exons, 4 introns and a 3' untranslated region (including the stop signals). The gene can be used to produce recombinant dCMP deaminase, which can be used to convert dCMP to dUMP. Also, the dCMP gene can be altered
                                                                                                                                                                                                                                                                                                     DNA encoding human deoxycytidylate deaminase recombinant deaminase Claim 2; Column 83-100; 58pp; English.
                                                                                                                                                                                                                                                                                                                                               (HEAL-) HEALTH RES INC Maley F, Maley GR, WG WPI; 97-244391/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The recombinant human kappa casein is produced in high yields by means of either a eukaryotic or prokaryotic expression system. It is used as a nutrient supplement in milk based products to provide a substantial improvement of the nutritional and biological value of the formulae, making it closer in similarity to human milk. It can also be used as a pharmaceutical.

Sequence 13104 BP; 4256 A; 2497 C; 2397 G; 3953 T;
                                                                                                                                                                         to mutagenesis. Sequence 20303 BP;
                                                                                                                                                                                                                                                                                                                                                                                      22-APR-1997.
10-JAN-1995; 370975.
10-JAN-1995; US-370975.
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WPI; 93-258675/32.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T71699
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant deaminase; dCMP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-AUG-1997 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptide(s) for use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SYMB-) SYMBICOM AB
                                                                                                                                                                                                  removed or mutated) to alter DNA replication in cells,
                                                                             289 CAGGAGTTCCAGACCAGCCTGG
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                                                                                                                    Local
                                                    CAGGAGTTCCAGACCAGCCTGG 15305
                                                                                                                                                                                                                                                                                                                                                                                                                                                       deoxycytidylate deaminase deoxycytidylate; deaminase
                                                                                                        l Similarity
22; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard; DNA;
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                                                                                                        Conservative
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                                                                                                                    6.4%;
                                                                                                                                                                                                                                                                                                                                                              Weiner KXB;
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                                                                                                 J.08;
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                                                                                                        Mismatches
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                                                                                                                   DB 1;
0.022;
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0.022;
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                                                                                                                               Length 20303;
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                                                                                                                    Query Match
Best Local
                                                                                                            Matches
                                                                      17247
                                                                                                                                                    Claim 3; Column 55-78; 58pp; English.

The present sequence encodes the human deoxycytidylate (dCMP) deaminase gene, which contains a 5' untranslated region (including the promoter), 5 exons, 4 introns and a 3' untranslated region (including the stop signals). The gene can be used to produce recombinant dCMP deaminase, which can be used to convert dCMP to dt Also, the dCMP gene can be altered (removed or mutated) to alter DR replication in cells, which may lead to mutagenesis.

Sequence 26784 BP; 7079 A; 5521 C; 6539 G; 7625 T;
                                                                                                                                                                                                                                                                      (HEAL-) HEALTH RES INC Maley F, Maley GR, We WPI; 97-244391/22.
                                                                                                                                                                                                                                                                                                                                                         misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human deoxycytidylate deaminase Recombinant deaminase; dCMP; ss.
Human c-fms oncogene
                         V20441 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   intron
       17-JUN-1998
                 V20441;
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22-APR-1997.
10-JAN-1995; 370975.
10-JAN-1995; US-370975.
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                                                                                                                   Local
                                                                      sapiens
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      (first entry)
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1318. 1177
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25468. .:
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25392. .:
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23741. .2
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1964. .2226
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                          DNA; 35100
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100.0%;
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                                                                                                          Score 22; DB; Pred. No. 0.0
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                          ВP
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                                                                                                                              DΒ
                                                                                                                     0.022;
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                                                                                                           0;
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RESULT
V83940
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Best Local
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human chromosome 10, 10q25.2 region. The sequence human chromosome 10, 10q25.2 region. The an unusual chromosomal marker referred to as mardel(10). The mardel(10) marker is mitotically stable and contains a functional neocentromere at a location regarded as non-centromeric. This neocentromere at a location regarded as non-centromeric including a neocentromere or its functional derivative or hybrid, that are able, in a compatible cell, of replicating, acting as extra-chromosomal element and segregating during cell division. The sequences can be used to construct artificial chromosomes for use in gene therapy comprising a replicable, segregating nucleic acid that confers a specific phenotype
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US5734039-A.
31-MAR-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytoplasmic oncogene or proto-oncogene selected from ras, raf, EGF-1, c-fms, c-ros, c-kit, c-met, c-trk, c-src, c-abl, bor-abl, c-for and c-yes. The second oligonucleotide is specific for a nuclear oncogene or proto-oncogene selected from myc, jun, c-ets, c-fos, c-myb, H-myb, c-rel, c-vav, c-ski, c-spi, cyclin Dl, PML/RAR alpha, AMLI/MTG8, E2A/prl and ALL-1/AF-4. The composition is used for treating cancer. The combination of antisense oligonucleotides has synergistically enhanced ability to inhibit growth of cancer cells.

Sequence 35100 BP; 8474 A; 8597 C; 9682 G; 8347 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anticancer composition comprising two anti-sense oligo:nucleotide(s) - targetting cytoplasmic and nuclear oncogene(s) Claim 1; Column 59-90; 92pp; English.
                                                                                                                                                                                                                                                                                        New isolated nucleic acid comprising neocentromere sequences from eukaryotic chromosome - used to produce replicable, segregating artificial chromosomes that can carry large amounts of DNA for ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NC-contig derived from mardel(10) on chromosome 10q25.2. Yeast artificial chromosome; YAC; probe; eukaryotic chromosome; replication; extra-chromosomal element; segregation; cell division; artificial chromosome; gene therapy; mardel(10); human artificial chromosome; transgenic; chromosome 10; 10q25.2; ss
                                                                                                                                                                                                                                                                                                                                                         (AMRA-) AMRAD OPERATIONS Cancilla MR, Choo K, Du S WPI; 99-009773/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
WO9851790-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents an oncogene from the present invention. The present invention describes a composition which comprises two antisense oligonucleotides. The first oligonucleotide is specific for a
                                                                                                                                                                                                                    The present sequence represents the NC-contig derived human chromosome 10, 10q25.2 region. The sequence cont
                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                                               13-MAY-1998; AU0352.
26-AUG-1997; AU-008791.
13-MAY-1997; AU-006784.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-MAR-1999 (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Calabretta B, Skorski T;
WPI; 98-229882/20.
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15-SEP-1994; US-306691.
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                                                                                                                                                                                                                                                                                therapy
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                                                                                                                                                                                                                                                          9; Fig 16A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
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; antisense oligonucleotide; c-fms; ds.
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                                                                                                                                                                                                                                                          540pp; English.
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100.0%;
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Pred. No.
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0.022;
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Best Local :
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                                                                                                                                                                                                                                                                       necentrowere at a location regarded as non-centroweric. This necentrowere maps to q25.2 on chromosome 10. The specification describes nucleic acid sequences derived from a eukaryotic chromosome, including a necentrowere or its functional derivative or hybrid, that are able, in a compatible cell, of replicating, acting as extra-chromosomal element and segregating during cell division. The sequences can be used to construct artificial chromosomes for use in gene therapy comprising a replicable, segregating nucleic acid that confers a specific phenotype on cells. Human artificial chromosomes can propagate in human cells and carry large amounts of DNA (e.g. therapeutic genes), and, being extra-chromosomal, they are not mutagenic. The artificial chromosomes are also useful for generation of transgenic plants and animals, in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  carry large amounts of DNA (e.g. therapeutic genes), and, being extra-chromosomal, they are not mutagenic. The artificial chromosomes are also useful for generation of transgenic plants and animals, in production of proteins and to make diagnostic reagents, e.g. for expression of cytokines, receptors and growth factors, or to increase the copy number of a gene in a cell. The constructs may also be used for functional and structural analysis of chromosomes. Sequence 80240 BP; 23102 A; 16537 C; 16747 G; 23846 T;
                                                                                                                                                                           production of proteins and to make diagnostic reagents, e.g. for expression of cytokines, receptors and growth factors, or to into the copy number of a gene in a cell. The constructs may also be used for functional and structural analysis of chromosomes. Sequence 80595 BP; 23183 A; 16613 C; 16824 G; 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents the HC-contig derived from normal human chromosome 10, 10q25.2 region. This region can be naturally mutated to produce an unusual chromosomal marker referred to as mardel(10). The mardel(10) marker is mitotically stable and contains a functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid comprising neocentromere sequences from eukaryotic chromosome - used to produce replicable, segregating artificial chromosomes that can carry large amounts of DNA for gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yeast artificial chromosome; YAC; probe; eukaryotic chromosome; neocentromere; replication; extra-chromosomal element; segregation; cell division; artificial chromosome; gene therapy; mardel(10); human artificial chromosome; transgenic; chromosome 10; 10q25.2; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   therapy Claim 8; Fig 6; 540pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AMRA-) AMRAD OPERATIONS PTY LTD. Cancilla MR, Choo K, Du Sart D; WPI; 99-009773/01.
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26-AUG-1997; AU-008791.
13-MAY-1997; AU-006784.
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19-NOV-1998.
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                                       289 CAGGAGTTCCAGACCAGCCTGG
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22; Conserv
                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            derived
                                                                               Conservative
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                                                                                                  Score 22;
Pred. No.
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                                                                                                                   Length 80595;
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T25057
ID T25057
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species; almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function of for recognising different cell types.

Sequence 158 BP; 46 A; 35 C; 44 G; 30 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 1759; 2245pp; Japanese.

A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection;
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11-NOV-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 95-206931/27.
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12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
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W09514772-A1.
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Result No. Minimum DB seq length: 0
Maximum DB seq length: 200000000 Title: Perfect score: Run OM nucleic - nucleic search, using sw model Database : Post-processing: Listing first 45 summaries Total number of hits satisfying chosen parameters: Searched: Scoring table: Sequence: 00000 ဂ ဂ O C 0000 on : size : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Score Query Match 0 US-09-065-672-4_COPY_1_276
276
1 CTAAGGCGTGCAAACAGAGC.... N_Geneseq_36:* OLIGO_NUC Gapop 60.0 , Gapext 60.0 October 3, 2000, 14:37:34; 311585 seqs, 125096042 residues Copyright CTAAGGCGTGCAAACAGAGC.....CGCGAGGCCGAGGCAGGAAG 11288 13565 14557 14557 1577 10090 20190 20190 110070 110070 110070 235033 237326 237326 237326 237326 1134 1134 1155 Length 338 406 541 632 688 688 2351 3523 3523 7146 GenCore version 4.5 (c) 1993 - 2000 Comp DВ V30406
V11854
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V57926 T25057 V87076 x22242 N902541 Q12226 V90303 Q59619 Q60129 Q60129 V90043 V88129 T72060 H SUMMARIES 임 Compugen Ltd Search time 114.21 Seconds (without alignments) 604.614 Million cell updates/sec 623170 Hereditary haemoch Hereditary haemoch Hereditary haemoch Human c-fos protei Human gene signatu Staphylococcus aur Human Duffy genomi Homo sapiens DNA f Nucleic acid seque CEA clone HindIII-Streptococcus pneu PEDF full length s Human SC3 DNA. Pro Sequence flanking Sequence flanking DNA encoding a hum Human brain Expres EST clone CW1510. EST clone FY354. N Continuation (2 of Enterococcus faeca Carcinoembryonic a Tumour rejection a CEA genomic clone. N-alpha-acetyltran EST clone DK113. N Human secreted pro DNA encoding N-alp Human gene signatu EST clone BJ66. Ne Description Human brain Expres

RESULT 2
V87076/C
ID V87076 standard; cDNA; 540 BI
AC V87076;
DT 27-APR-1999 (first entry)
DE EST clone BJ66.

ВP

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Query Match Best Local Matches

1 Similarity 19; Conserv

Conservative

6.9%; Score 19; DB 100.0%; Pred. No. 0. tive 0; Mismatches

DB 1; 0.6;

0; Indels Length 158;

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Gaps

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No.	A single-stran given in T19 human genomi sequences we from various 3'-end of mR untranslated all the 3'-ois construct different mR The appearan determined (sequences) a recognising Sequence	T25057 standard; T1-NOV-1996 (fi) T2-NOV-1994; T2-NOV-1993;	
) T	lle-stranded in T19001 in T19001 cos were ariment but cos were ariment of mRNA il stated see a criminate in TRNAs cent mRNAs cent mRNAs pearance pearance itself dispersion of the cos were than the cos was a satising different to the cos was a satising different to the cos was a satising different mRNAs cos was a satising different to the cos was a satising different manual transferent manua	7 725057 standard; c T25057; standard; c T25057; I1-NOV-1996 (firs Gene signatur; me human gene signatur Gene signatur; me human; cloning; ma cell typing; abnor Homo sapiens. W0951472-A1 01-JUN-1995. U1-NOV-1994; J0191 11-NOV-1994; J0191 12-NOV-1993; JP-351 (MATS/) MATSUBARA (OKUB/) OKUBO K. Matsubara K. Okub WPI; 95-206931/27. Identifying gene s for diagnosis of a reflects relative	166
	A single-stranded DNA (or its double-stranded DNA) which com given in T19001-T26337 and whi human genomic DNA, CDNA or mRNA sequences were obtained from 3 from various human tissues; sy 3'-end of mRNA by using poly(T untranslated sequence is unique all the 3'-oriented CDNAs hybris constructed so as to reflect different mRNAs in the particue. The appearance frequency of a determined (esp. using primers sequences) as a means of diagn recognising different cell typ sequence 158 BP; 46 A;	andard; cDNA to mR 96 (first entry) e signature HUMGS0 ature; messenger R oning; mapping; no ng; abnormal cell ensAl. 93; JP-355504. 93; JP-355504. ATSUBARA K. KUBO K. K. Okubo K; KOBO K. K. Okubo K; KOBO K. K. Okubo K; 06931/27. ng gene signatures osis of abnormal cell relative abundance	
		cDNA to mRNA; st entry) ure HUMGS0718 lessenger RNA; lapping; non-b prmal cell fun 155504. kK. bbo K; signatures in abnormal cell abnormal cell	258 1 269 1 269 1 271 1 271 3 303 1 341 1 341 1 350 1 358 1
	its complise which is comprise which is mRNA is mRNA is mRNA is of joint of the compression of the complete acceptance and faginasing types.	NA; 7188 NA; n-bi func	Q61087 T22202 Q60189 T26324 V86324 V88486 V88486 Q61371 Q61371 Q61371 Q61371 Q61371 Q60394 Q61360 ALIGNMENTS
;	ementary strand or the coss one of the 7837 "GS" see able to hybridise to par claimed. The GS (Gene Siguected CDNA libraries prepartis of cDNA was initiated the sole primer. Since the a particular mRNA species with specific mRNAs. Eacl urartely the relative abundissue from which it was doing GS in a cDNA library can probes derived from the GS abnormal cell function or abnormal cell function of abnormal cell function of	lative rary; d , by pr mRNA i	NTS
	y strand or the cor f the 7837 "GS" seq o hybridise to part The GS (Gene Signa NA libraries prepa, NA was initiated fi a primer. Since the ular mRNA species, eecific mRNAs. Each the relative abund com which it was de- icDNA library can library ca	ce; s;	Hum Hum Hum Hum Hum EST Hum Hum Hum Hum Hum Hum
o	of the 7837 "GS" sequences to hybridise to part of ed. The GS (Gene Signature) cDNA libraries prepared cDNA was initiated from the sle primer. Since the 3'-icular mRNA species, almost specific mRNAs. Each library y the relative abundance of from which it was derived. I a cDNA library can be ederived from the GS mmal cell function or for 14 G; 30 T;	ce; frequency; s; detection; sidetection;	Human brain Expres Human gene signatu Human brain Expres Human gene signatu EST clone HOl07. N Human brain Expres EST clone EN10. Ne Human brain Expres Human gene signatu Human gene signatu Human brain Expres Human brain Expres

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PT New polynucleotides encoding human secreted proteins - derived from PT e.g. human blood, kidney, foetal lung, placenta, testes, brain, provary, pituitary, retina and colon cDNA libraries Claim 1; Page 444; 633pp; English.

CC Phis sequence represents an expressed sequence tag (EST), and is a polynucleotide of the invention. The polynucleotides of the invention are color polynucleotide of the invention. The polynucleotides of human tissue sources. The EST sequences isolated from a variety of human tissue sources. The EST sequences and proteins encoded by them are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and color animals, although no supporting data is given. Suggested activity, the continual color in the supporting data is given suppressing activity, haemostatic condition in the color of the co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local :
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  22-JUL-1997;
22-JUL-1997;
22-JUL-1997;
18-AUG-1997;
18-AUG-1997;
18-AUG-1997;
18-AUG-1997;
18-AUG-1997;
                                                                                                                                                                                                                                                                                       15-JUL-1998;
18-AUG-1997;
16-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                             duman secreted protein gene 32 clone HJABC16.
Human; secreted protein; gene therapy; protein therapy; cancer; weight;
tumour; chromosome mapping; forensic; haematological disease; allergy;
inflammation; cell proliferation; viral infection; wound healing;
modulation; appetite; behaviour; food additive; preservative; ss.
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Sequence
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Agostino MJ, Jacobs K, Lav
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10-APR-1998; U06954
10-APR-1997; US-835
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                                                                                                                                                                                                                                                                                                                                                                                                Homo
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16-JUL-1997;
                                                                                                                                                                                                          16-JUL-1997;
16-JUL-1997;
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16-JUL-1997;
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US-052661.
US-052870.
US-052871.
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US-052873.
US-052875.
US-052875.
US-053440.
US-053441.
US-053442.
US-055683.
US-055724.
US-055724.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      secreted protein; haematopoiesis regulator; inhibin; tumour invasion suppressor: EST: h
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Pred. No. 0.62;
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asis; gene therapy; thrombolysis;
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Best Local 9
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The invention relates to nucleic acid sequences (X22211 to X22282)

The invention relates to nucleic acid sequences (X22211 to X22282)

encoding human secreted proteins (Y01383 to Y01454). The secreted protein gene sequences are deposited with the ATCC under deposit number ATCC 209138, 209139 or 209141. Host cells containing vectors comprising the nucleic acid sequences are used for the recombinant expression of the secreted proteins. The polynucleotide and amino acid sequences are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Pathological conditions can be also diagnosed by determining the amount of the new polynucleotides. The nucleic acid sequences, or its fragments, are useful for chromosome identification and sequences, or its fragments, are useful for chromosome identification and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequences, e.g. autoimmune or haematological diseases, allergy, inflammation, cancer or other forms of cell proliferation, viral or o infections. The sequences may also be useful in wound healing, to modulate differentiation of embryonic stem cells, to modulate weight, appetite, behaviour etc. and as food additive or preservative. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mapping; as antisense and triplex-forming therapeutics; in gene therapy; for (forensic) identification of individuals; as molecular weight markers; to identify related sequences or specific mRNA; in preparation of oligomers and to raise anti-DNA antibodies. Antibodies are useful as immunoassay reagents (including for in vivo imaging) and therapeutically to inhibit or activate particular polypeptides. A very wide range of disorders may be treated with the polynucleotide and polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present sequence represents a gene encoding a human secreted pr (see descriptor line for gene number and clone identification). Sequence 702 BP; 187 A; 154 C; 174 G; 183 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Greene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-AUG-1997; US-055952
18-AUG-1997; US-055985
18-AUG-1997; US-055989
18-AUG-1997; US-056359
                                                                    misc_feature
                                                                                                                                      misc_feature
                                                                                                                                                                         misc_feature
                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                             N-alpha-acetyl transferase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC.
Duan R, Feng P, Ferrie AM, Florence KA,
                                                                                                                                                                                                                                           protein N-acetylation.
                                                                                                                                                                                                                                                                             DNA encoding N-alpha-acetyl
                                                                                                                                                                                                                                                                                              N90541;
28-NOV-1989 (first entry)
                                                                                                                                                                                                                                                                                                                                N90541 standard; recombinant DNA; 2703
                                                                                                                                                                                                                                                                                                                                                                                                                      441 TTCGGGAGGCCGAGGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                     255 TTCGGGAGGCCGAGGCAGG 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hu J, Ni J, Rosen CA, Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                  /*tag= c
542. .566
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971. .
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479. .515
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338. .392
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1007.
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                                                                                                                                                                                                                                                                               transferase.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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diseases and ident
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
0.62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Young
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misc_feature

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AC Q122
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                                                                                                                                                                                                                                                                      012226 standard; cDNA; 2724 BP.
012226;
02-AUG-1991 (first entry)
N-alpha-acetyltransferase; amino
N-alpha-acetyltransferase; amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 8; Page 50; Fig 12b-e; 72pp; English.

DNA encodes N-alpha-actyl transferase, used for catalysing N-acetylation of peptides/proteins, eg to stabilise pharmaceuticals or to induce herbicide resistance in plants. Features a - n are fragments resulting from exonuclease III deletion. See also P91070.

Sequence 2703 BP; 943 A; 489 C; 530 G; 741 T;
Mutant N-alpha-acetyl-transferase - produced from Saccharomyces cerevisiae for use in amino acid sequence determn. Disclosure; Fig 1; 77pp; English.
The AAAl gene is located on chromosome IV and is positioned adjacent to the 5' flanking sequence of the SIR2 gene. Cells contg. a mutated AAAl gene lack N-alpha-acetyltransferase activity and are used to express, in vitro a recombinant protein peptide lacking an acetyl gp. at the alpha-amino gp. or to produce heterologous proteins. The proteins produced have altered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-AUG-1989.
07-FEB-1989; U00471.
08-FEB-1988; US-153361.
14-DEC-1988; US-284344.
(GEHO) The General Hospital Corporation.
5mith JA, Lee FUS.
WPI: 89-24908/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New pure N-alpha-acetyl transferase and DNA encoding i acetylation of proteins and peptides, eg to stabilise or induce herbicide resistance in plants.
                                                                                                                                                                                                                                       Key
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                                                                                                                          25-OCT-1989; US-426381.
(GEHO-) GEN HOSPITAL CORP.
Smith JA, Lee FJS;
WPI; 91-164219/22.
                                                                                                                                                                         16-MAY-1991.
15-OCT-1990; U05883
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1088.
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                                                                                                                                                                                                               N-alpha-acetyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 18;
Pred. No.
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                                                                                                                                                                                                                                                                          acid
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e pharmaceuticals
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                           protein or
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Best Local
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene therapy; ss. Homo sapiens. W09845436-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, activin/inhibin activity, chemotactic/chemokinetic activity, haemastopoiesis regulating chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, the polynucleotide may also be useful for gene therapy. Sequence 332 BP; 71 A; 83 C; 84 G; 94 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 substrate specificity and thermal stability. sequence of such proteins and peptides can be Sequence 2724 BP; 953 A; 491 C; 5:
                                                                                                                                                                                                            19/c
Q59619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polynucleotides encoding human secreted proteins - derived e.g. human blood, kidney, foetal lung, placenta, testes, brain, ovary, pituitary, retina and colon cDNA libraries. Claim 1; Page 497; 618pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Agostino MJ, Jacobs K, Lavallie Racie LA, Spaulding V, Treacy M; WPI; 99-070077/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; secreted protein; expressed sequence tag; EST; haematopoiesis; tissue growth; activin; inhibin; chemotaxis; chemokinesis; haemostatic; receptor; ligand; thrombolytic; anti-inflammatory; cadherin; anti-tumou
                        Homo sapiens. W09316178-A.
                                                                                                   Human brain Expressed Sequence Tag EST01488.
Gene transcription product; genetic markers; tagging; in vivo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The polynucleotide, which is a secreted EST, and the encoded pare predicted to have useful biological activities which would
                                                                             transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a human expressed sequence tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-OCT-1998.
10-APR-1998; U06955.
10-APR-1997; US-838821.
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                                                                                                                                                          16-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GEMY ) GENETICS INST INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     168 TGCTTTTCTCTCTAATAA 185
                                                                                                                                                                                                                                                                                                                                              285
                                                                                                                                                                                                                                                                                                                                                                                               258 GGGAGGCCGAGGCAGGA 274
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                                                                                                                                                                                                               standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      l Similarity
17; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
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                                                                                                                                                                                                               cDNA;
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                                                                             locations; chromosomes;
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7;
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533 G; 74
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                                                                                      Query Match
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The Expressed Sequence Tag was isolated from a human brain cDNA library as part of a large set of ESTs which can be used as markers for human genes transcribed in vivo. They can be used to facilitate tagging of most human genes, for mapping locations of expressed gene on chromosomes, for individual or forensic identification, for mappil locations of disease-associated genes, for identification of tissue type, and for prepn. of antisense sequences, probes and constructs. EST01488 has a "poor" coding probability as evaluated using the coding-region prediction program CRM. See also QS5041-Q61440.

Sequence 338 BP; 77 A; 106 C; 67 G; 87 T;
                                                                                                                                                          type, and for prepn. of antisense sequences, probes and constructs. EST02116 has a "poor" coding probability as evaluated using the coding-region prediction program CRM. See also 059041-061440. Sequence 406 BP; 74 A; 97 C; 110 G; 124 T;
                                                                                                                                                                                                                             The Expressed Sequence Tag was isolated from a human brain cDNA library as part of a large set of ESTs which can be used as markers for human genes transcribed in vivo. They can be used to facilitate tagging of most human genes, for mapping locations of expressed genes on chromosomes, for individual or forensic identification, for mapping locations of disease-associated genes, for identification of tissue
                                                                                                                                                                                                                                                                                                                                          markers for human genes transcribed of most human genes sxample 4; Page 286; 500pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                        Adams MD,
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Gene transcription product; genetic markers; tagging; in vivo;
transcription; mapping; locations; chromosomes; chromosomal; s
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12-FEB-1993; U01294.
12-FEB-1992; US-837195.
(USSH) US DEPT HEALTH.
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Enriched oligonucleotides and corresp. sequences - used markers for human genes transcribed in-vivo, facilitate
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12-FEB-1992; US-837195.
(USSH) US DEPT HEALTH & HUMAN SERVICE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-MAR-1994
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les 17; Conserv
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ATTTCGGGAGGCCGAGG 21
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Matches 17
                                 New polynucleotides encoding human secreted proteins - derived from e.g. human blood, kidney, foetal lung, placenta, testes, brain, ovary, pituitary, retina and colon cDNA libraries claim 1; Page 292; 641pp; English.

The present sequence represents an expressed sequence tag (EST), and is a polynucleotide of the invention. The polynucleotides of the invention are all secreted EST sequences isolated from a variety of human tissue sources. The EST sequences and proteins encoded by them are predicted to the invention of the invention of the invention are all secreted EST sequences and proteins encoded by them are predicted to the invention of the 
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Claim 1; Page 413; 618pp; English.

The present sequence represents a human expressed sequence tag (EST) The polynucleotide, which is a secreted EST, and the encoded proteir are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, haematopoiesis regulating activity, tissue growth activity, activin/inhibin activity.
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10-APR-1998; U06956.
10-APR-1997; US-837312.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Expressed sequence tag; secreted protein; haematopoiesis regulator; tissue growth; activin; inhibin; tumour invasion suppressor; EST; hichmotaxis; chemokinesis, haemostasis; gene therapy; thrombolysis; receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
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15-OCT-1998.
10-APR-1998; U06955.
10-APR-1997; US-838821.
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WO9845437-A2.
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which would make them suitable
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TREASON OF THE PROPERTY OF THE
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CC Group B: D65464, D65306, D65258, D65265, D65105 and D651001.

CC The absence of the genotype indicates the likelihood of the presence of the HH mutation of genotypes characteristic of heteroxygous carriers and 25 CC the HH mutation in their genomic DNA. The potential for 25 CC the control of the genotypes with the effectiveness of interferon the interferor with the effectiveness of interferon the interferon and a modividual interferes with the effectiveness of interferon the interferon and 25 CC the interferon the interferon and 25 CC the interferon the interferon the interferon and 25 CC the interferon the interferon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       using primers based on novel microsatellite repeat flanking sequences or on base-pair polymorphisms HHP-1, HHP-19 or HHP-29 Claim 24, Fig 1P, 67pp; English.

The sequences given in T72045-67 represent portions of the genome surrounding several markers of the invention. The markers were identified using the series of primer pairs given in T71973-2044 which were used to determine the presence or absence of the common hereditary hemochromatosis (HH) gene mutation in an individual.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence flanking marker 950-2 in HH region of chromosome 6p2.1. Primer; polymerase chain reaction; amplify, hereditary haemochromatosis; HH; mutation; HH-associated allele; base-pair polymorphism; HHP-1; HHP-19; HHP-29; microsatellite repeat allele; genetic marker; interferon treatment; hepatitis C infection; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MERC-) MERCATOR GENETICS INC.
Drayna DT, Feder JN, Gnirke A,
Wolff RK;
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08-MAY-1995; US-436074.
15-NOV-1995; US-559302.
09-FEB-1996; US-599252.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-AUG-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                               responsiveness
Sequence 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9635802-A1.
                                                                                                                                                                                                                                                            treatment for hepatitis C infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             256 TCGGGAGGCCGAGGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38
                                                                            Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          thrombolytic activity, receptor/ligand activity, anti-inflammatory ivity, cadherin/tumour invasion suppressor activity, tumour inhibit ivity. The EST sequences are also stated to be useful for gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCGGGAGGCCGAGGCAG
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   l Similarity
17; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the common hereditary haemochromatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , preventing although no
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                   of
BP
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                                                                                                                                                                                   interferon; 213 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or ameliorating medical conditions in humans supporting data is given. Suggested activitie
                                  6.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
   0
                                  Score 17;
Pred. No.
                                                                                                                                                                           fection. By diagnosing this potential, treatment may be evaluated.
155 C; 137 G; 171 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         186
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                                  DB 1;
7.1;
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7.1;
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                                                                        Length 688
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mutation
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Mismatches

Indels

0;

Gaps

0;

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RESULT
X30406
ID X3
AC X3
AC X3
DT 1/
DE DI
KW S
KW S
KW C
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08-MAY-1996; U06583.

08-MAY-1995; US-436074.

15-NOV-1995; US-559302.

09-FEB-1996; US-599252.
                                                                                                                                                                                                                                                                                                                                         A and optionally of group B:
Group A: 1909, 1884, 1A2, 1E4, 24E2, 2B8, 3321-1, 4073-1, 4440-1, 4440-2, 731-1, 5091-1, 3216-1, 4072-2, 950-1, 950-2, 950-3, 950-4, 950-5, 950-6, 950-8, 63-1, 63-2, 63-3, 65-1, 65-2, 373-8, 373-29, 68-1, 241-6, 241-29; Group B: D6S464, D6S306, D6S258, D6S265, D6S105 and D6S1001.

The absence of the genotype indicates the likelihood of the presence of the HH mutation. Knowledge of the new genetic markers allows the definition of genotypes characteristic of heterozygous carriers and homozygotes having a HH mutation in their genomic DNA. The potential for HH in an individual interferes with the effectiveness of interferon treatment for hepatitis C infection. By diagnosing this potential, the responsiveness of interferon treatment may be evaluated.

Sequence 688 BP; 213 A; 155 C; 137 G; 171 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 24; Fig 1P; 67pp; English.

The sequences given in T43925-55 represent portions of the genome surrounding several markers of the invention. The markers were identified using the series of primer pairs given in T71901-72 which were used to determine the presence or absence of the common hereditary haemochromatosis (HH) gene mutation in an individual. The method comprised assessing genomic DNA from an individual for the presence or absence of the HH-associated allele of the single base-pair polymorphism HHP-1, HHP-19 or HHP-29, and/or at least one non-optional marker comprising the following microsatellite repeat alleles of group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drayna DT Wolff RK;
          DNA encoding a human secreted protein.
Secreted protein; cancer; tumour; neurodegenerative disorder; developmental abnormality; foetal deficiency; blood disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Diagnosing and genotyping of hereditary haemochromatosis using primers to detect specific polymorphisms of the HH chromosome 692.1 or novel microsatellite markers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HHP-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T43940
                                                                     14-MAY-1999
                                                                                       X30406;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MERC-) MERCATOR GENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9635803-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        interferon treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HH; mutation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-AUG-1997
                                                                                                       X30406
                                                                                                                                                                                          116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  258
   disorder;
                                                                                                                                                                                         GGGAGGCCGAGGCAGGA 132
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                                                                                                                                                                                                                                                            l Similarity
17; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; DNA;
                                                                                                       standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polymerase chain reaction; amplify; hereditary haemochromatosis; ation; HH-associated allele; base-pair polymorphism; HHP-1; HHP-29; microsatellite repeat allele; genetic marker; ron treatment; hepatitis C infection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Feder JN,
                                                                                                                                                                                                                                                            Conservative
                                                                   (first entry)
                                                                                                       DNA;
                                                                                                                                                                                                                                                     6.2%; bu
100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gnirke A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  274
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                                                                                                       ВP
                                                                                                                                                                                                                                                                                          Score 17;
                                                                                                                                                                                                                                                                          Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kimmel
                                                                                                                                                                                                                                                                                            DB 1;
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                                                                                                                                                                                                                                                                                            Length 688;
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hepatic
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 disease;
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RESULT
V11854
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Best Local S
Matches 17
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05-AUG-1997; US-055309

05-AUG-1997; US-055310

05-AUG-1997; US-055316

05-AUG-1997; US-055386

05-AUG-1997; US-055386

05-AUG-1997; US-055396

18-AUG-1997; US-055986

19-AUG-1997; US-056365

19-AUG-1997; US-056365

19-AUG-1997; US-056370

19-AUG-1997; US-056370

19-AUG-1997; US-056371

19-AUG-1997; US-056371

19-AUG-1997; US-0563731

19-AUG-1997; US-0563731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-AUG-1997; US-056732.
05-AUG-1997; US-054798.
05-AUG-1997; US-054803.
05-AUG-1997; US-054804.
05-AUG-1997; US-054806.
                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated human genes encoding secreted polypeptides - useful for diagnosis and treatment of pathalogical diseases (laim 3; Page 269; 331pp; English.)
The specification describes secreted proteins and their corresponding polynucleotides which are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Pathological conditions can also be diagnosed by determining the amount of the secreted polypeptides in a sample or by determining the presence of mutations in the polynucleotides. Specific uses are described for each of the products, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, developmental abnormalities and foetal deficiencies, blood disorders, CNS disorders, diseases of the immune system autoimmune diseases bearing and recal
14-SEP-1998 (first entry)
Human Duffy genomic DNA se
Duffy gp-Fy; FY*B gene; bl
                                                      V11854 standard; DNA; 3523 BP
V11854;
                                                                                                                                                        2199
                                                                                                                                                                                                                                                                                                      prostate diseases, asthma, disorders involving osteoclasts such as osteoporosis, arthritis or malignancies, diseases of testes, lung or thymus, digestive/endocrine disorders, infections and AIDS. The polypeptides are also useful for identifying their binding partners. Seguence 2351 BP; 702 A; 446 C; 518 G; 675 T;
                                                                                                                                                                                                                                                                                                                                                                                        diseases of the immune system, autoimmune diseases, hepatic and renal disease, diabetes, inflammation, allergies, ischemic shock, Alzheimer and cognitive disorders, schizophrenia, cardiovascular disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; Y10885.
New isolated human genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Olsen HS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-AUG-1997;
05-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens. W09907891-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prostate disease; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           renal disease; diabetes; inflammation; allergy; ischemic shock; Alzheimer's; cognitive disorder; schizophrenia; cardiovascular disorder;
                                                                                                                                                                                        258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ver LA, Ebner R, Ferrie AM
in HS, Rosen CA, Ruben SM,
99-167452/14.
                                                                                                                                                                                      GGGAGGCCGAGGCAGGA 274
                                                                                                                                                      GGGAGGCCGAGGCAGGA 2215
                                                                                                                                                                                                                         Similarity
17; Conserv
                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-054807.
US-054808.
ic DNA sequence (FY*B).
gene; blood group; blood typing; human;
                                                                                                                                                                                                                                       6.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           osteoporosis; arthritis; ss.
                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                     Score 17;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Soppet
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7.4;
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Young PE,
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                                                                                                                                                                                                                                                       Length 2351;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or ameliorating
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                                                                                                                                                                                                                                                                                                                                                                                                            Alzheimer's
                                                                                                                                                                                                                                                                                                                                                         lung or
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RESULT
V27017
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transgenic animal to express a first form of a polymorphic protein encoded by a first allele of a gene encoding the protein; constructing a second transgenic animal to express a second form of the polymorphic protein encoded by a second allele of the gene encoding the protein; and immunising the first transgenic animal with cells from the second transgenic animal to induce an immune response in the first transgenic animal yielding an antibody specific for an epitope peculiar to the second form of the polymorphic protein. The invention is particularly advantageous in the context of making MAbs and derivative reagents specifically identifying polymorphic blood group proteins, such as the Duffy and the polymorphic blood group proteins, such as the Duffy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (FY*B) used to produce transgenic mice. It was obtained by PCR amplification using FY-specific primers (see V11852-53). The amplified fragment was cloned in the pBluescript vector, and a purified DNA fragment containing the FY*B gene was microinjected into the male pronucleus of fertilised eggs of the B6/CBA F1 mouse. Transgenic mice were obtained. The invention relates to a method for making monoclonal antibodies (MAbs) having pre-defined specificity to an epitope characteristic of, or unique to, a single form of a polymorphic protein. This includes constructing a first transgenic animal to protein. This includes constructing a first transgenic animal to protein.
                                                                                                                                                  Homo sapiens DNA fragment containing FY*B coding sequence gp-FY protein; Fyb71-81; duffy blood group; antigen; alpha alternative splicing; RBC; red blood cell; malaria; treatm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polymorphic protein - useful in blood typing etc.
Example 1; Fig 3A-B; 43pp; English.
This nucleotide sequence comprises a Duffy genomic DNA sequence
                                                                                                                                                                                                                                   V27017;
11-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reid ME;
WPI; 98-297923/26
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                  14-NOV-1997; U21067.
15-NOV-1996; US-749543
                                                                                                    WO9821224-A1.
                                                                                                                                                                                                                                                                                 V27017 standard; DNA; 3523 BP
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15-NOV-1996; US-749527
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  NEW
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YORK BLOOD CENT INC.
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3501. 3501
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1661
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Pred. No.
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cell; malaria; treatment; ss
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7.4;
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Chaudhuri A, Pogo OA;
WPI; 98-297854/26.
Nucleck acid encoding gp-Fy, Duffy antigen proteins - used to prevent vivax malaria and to regulate erythrocyte, neural or renal function
Example 15; Fig 13; 87pp; English.
The sequence is that encoding a major subunit of the Duffy blood group antigenic system, the gp-Fy proteins. The gp-Fy proteins are gp-Fy alpha and gp-Fy beta which are produced from the same gene via a mRNA splicing mechanism. It contains the major receptor by which plasmodium vivax enters red blood cells (RBC) and causes malaria. The proteins are thus useful in preventing malaria and in regulating RBC, renal and neural function. The protein or certain fragments of it, may also be used to generate antibodies, complementary peptides and drugs modelled on their tertiary structure, useful in the same way.

Sequence 3523 Bp; 720 A; 1042 C; 806 G; 955 T;
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PI DR PT DR

Search completed: October 3, 2000, 14:37:36 Job time: 5195 sec

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4.5 Compugen Ltd

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Title:
Perfect score:
Sequence:
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Maximum DB seq length: 200000000
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   Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            311585 seqs, 125096042 residues
   GenCore version Copyright (c) 1993 - 2000
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  840
1363
2310
2676
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11534
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24026
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24026
 V33947

Q95493

T25848

V39298

V115455

Q14851

Q14851

Q14850

T71699

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T71699

T71699

T7169666

V201491

V83940

T1750

T17516

T17513

T17514

T17516

T17516

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T17516
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HC-contig derived
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Human RAD54 nuclei
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PN FT FK W

Homo sapiens. Key cds

Location/Qualifiers 3312. .3947 /*tag= a

shock; lymphoma; eczema; ss.

W09515084-A.

REST Q954 ID AC DT DE KW	Qu Ma Qy	###80000000000000000000000000000000000	RESUL X3394 AC DT DT DE DE CKW KKW KKW OS PD PD PD PD PD PD PD PD PD PD PD PD PD		
RESULT 2 Q95493/c ID Q95493; AC Q95493; DT 21-NOV-1995 DE Human Cdn-2; KW Cdn-2; apopt KW autoimmune d	uery Mai sst Loca tches 289 (New is Claim This sto expens repres genes be use also be use associble use sequent	147 147 233947 333947 333947 333947 333947 333947 333947 33947 3407 407 407 407 407 407 407 407 407 407	4. U	00000000000000000000000000000000000000
standard; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;	tch al simi. 26; CAGGAGT	years by (cig or control of contr	7 standa 4-1999 4-1999 inducib inducib sciral tiscreenii screenii	2	21 21 21 21 21 21 21 21 21 21 21 21 21 2
lard; (fir DNA. DOSis	larit Conse TCCAG	huma huma e 143 e rep y bot the cr cig tha for for reatm feath feath	(fir (fir nduci nduci nduci nduci 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		
DNA; 6 st ent modula	7.5%; Scral Similarity 100.0%; P. 26; Conservative 0; CAGGAGTTCCAGACCAGCCTGGGCAACCAGCCTGGGCCAACCAGCCAG	-147; 11 resents h HCMV s). The presence s). The the devicents widenist dminist dminist driin, d	DNA; 321 st entr; ble gen ne; cig y; anti s. 59725. 59725. CETON. CETON.	670167	12 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
511 B ry) tor; erfus	5%; .0%; TGGG	84pp a h and inv e of pro hera elop thou erin	9) y) ; hu -HCM		
P. adoptive immunotherapy; ion injury; hepatitis,	Score 26; DB 1; Length: Pred. No. 0.00019; 0; Mismatches 0; Ind SCAA 314	unman gene of the inventice interferon (IFN), designate from (IFN), designate that wention also relates to gether than the can be used to obtain the concomitant toxicit the concomitant toxicit the concomitant toxicit the concomitant graph in the concomitant toxicit the concomitant toxicit the concomitant toxicit the concomitant toxicit the gament of drug screening.	RESULT 1 X33947 ID X33947 standard; DNA; 3200 BP. AC X33947, DT 30-JUN-1999 (first entry) DE Human HcMV inducible gene, SEQ ID NO 21. KW HCMV inducible gene; cig; human; human cytomegalovirus; interferon; KW anti-viral therapy; anti-HCMV therapy; detection; diagnosis; KW drug screening; ds. OS Homo sapiens. PN W09913075-A2. PD 18-MAR-1999; U18638. PF 08-SEP-1997; US-059725. PR 22-SEP-1997; US-059180. PA (UYPR-) UNIV PRINCETON. PI Cong J, Schenk T, Zhu H;	ALIGNMENTS	717519 717521 717522 717523 717524 717526 717527 717529 717529 717529 717529
therapy: HIV;	1 3200; dels 0; Gaps 0	n, that is induced ated HCMV-inducible enes that are led HCMV-repressible ain agents which can. My therapy. They can allow for higher y normally products can also 857 T;	s; interferon; ignosis;	Murared BRCA1 geno	Mutated BRCAl geno BRCAl genomic sequ BRCAL human breas

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30-NOV-1994; U13930.
30-NOV-1993; US-160067.
07-OCT-1994; US-320157.
(LXRB-) LXR BIOTECHNOLOGY INC.
Barr PJ, Kiefer MC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          using a 950 bp fragment of Cdn-1 cDNA. Expression of Cdn-2 in mouse progenitor B-cell FL5.12 cells decreased IL-3-induced apoptosis. The Cdn-2 protein displayed 97% amino action with Cdn-1 (R77876).

Sequence 6511 BD.
                                                                                                                                                                    Claim 1; Page 1942; 2245pp; Japanese.
A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAS. Each library is constructed on the float the contract of the contract o
                     is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying gene signatures in 3'-directed human cDNA library -
for diagnosis of abnormal cell function, by preparing cDNA that
reflects relative abundance of corresp. mRNA in specific human
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WPI; 95-215106/28.
P-PSDB; R77877.
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12-NOV-1993; JP-355504
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0.0022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Expression of Cdn-2 decreased IL-3-induced 97% amino acid identity
  ç;
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  19
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                                                                                                                                                    of
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Query Match
Best Local Similarity

6.6%;

Score Pred

23; No.

DB 1; 0.0064;

Length

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RESULT 4
V39298;
DY 16-SEP-
DF 16-SEP-
DE Human R:
KW Human;
KW Weiner's
KW X-linkee
KW gene the
OS Homo sal
PH EP-8443
PD 17-MAY-
PF 10-NOV-
PR 13-NOV-
P
                                                                                                                                                                                                                                                                                                                                                           RESULT
T15455
ACC DT DE KW KW KW PN PN PR PR
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Best Local Similarity
Matches 22; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA sequence of at least 15 and no more than 30 consecutive bases of the DNA sequence encoding hRAD54. hRAD54 is a gene thought to be present in tumours that display allelic imbalance at 1732, the chromosomal band identified as one of four minimal regions of chromosome 1 deletion in breast carcinomas. hRAD54 is useful for production of proteins, inter alia, that have been identified as novel hRAD54 homology between the amino acid sequence given in W62186 and known amino acid sequences such as yeast RAD54. hRAD54 proteins are used in the treatment of cancer, including Xeroderma Pigmentosum and Bloom syndrome, Werner's syndromes and X-linked mental retardation with alpha-thalassaemia syndrome and
                                                                                                                                           Lung cancer specific antigen HCAVIII promoter region genomic, Non-small cell lung cancer; NSCLC; tumour marker; HCAVIII; carbonic anhydrase; diagnosis; therapy; promoter; DNA probe; fluorescent in situ hybridisation; ds.
                                                                                                                                                                                                                                                                    T15455;
23-APR-1996
                                                                                                                                                                                                                                                                                                                               T15455 standard; DNA; 1363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       breast cancer. hRAD54 polynucleotides are also useful for detecting complementary nucleotides for use as a diagnostic agent, especially useful for diagnosis of disease or susceptibility to diseases. hRAD
                                                           01-FEB-1996.
                                                                                   Homo sapiens. W09602552-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polynucleotide, proteins, agonists and antagonists which are proteins
are useful in gene therapy.
Sequence 840 BP; 190 A; 200 C; 221 G; 229 T; |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a specifically claimed partial nucleic acid sequence encoding human RAD54 (hRAD54). A method for analysing a sample for mutation of DNA encoding hRAD54 has been developed using a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human hRAD54 DNA and polypeptide - and agonists, antibodies, antagonists, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Croce CM, Fishel RA, Rasio WPI; 98-274189/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EP-844305-A2.
27-MAY-1998.
10-NOV-1997; 308998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; RAD54; hRAD54; cancer; xeroderma pigmentosum; Bloom syndrowerner's syndrome; ATR-X; diagnosis; detection; SNF2 superfamily; X-linked mental retardation with alpha-thalassemia syndrome; tumo
19-JUL-1995;
19-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 28; 64pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SMIK ) SMITHKLINE BEECHAM CORP.
(UYJE-) UNIV JEFFERSON THOMAS.
Croce CM, Fishel RA, Rasio D, Robbins DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene therapy; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-NOV-1996; US-030676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 150
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ilarity 100.0%;
Conservative
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U09145.
US-276919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 22;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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BB
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.023;
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DR WPI, 96-105844/11.

PT Nucleic acid encoding the lung cancer specific antigen HCAVIII -
PT useful for diagnosis and treatment of non-small cell lung cancer
PS Claim 53; Page 62-63; 87pp; English.

CA genomic clone (T15455) was isolated that constitutes the putative
promoter of the HCAVIII gene (see T15448), and probably contains
C transcription regulatory elements directly implicated in expression
C fHCAVIII, a cell surface antigen which is highly specific for
C non-small cell lung carcinoma and which has features in common with
CC human carbonic anhydrases. The clone was obtd. by PCR amplification
CC using a primer pair (T15456-57) based on the putative exon 6 of the
CC HCAVIII gene. A DNA probe comprising the genomic clone plus
CC flanking sequences was used for fluorescent in situ hybridisation.
SO Sequence 1363 BP; 352 A; 382 C; 369 G; 260 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-NOV-1991.
25-APR-1991; J00557.
27-APR-1990; JP-113146.
31-JUL-1990; JP-204438.
14-SEP-1990; JP-245256.
28-DEC-1990; JP-415801.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q14851 stand
Q14851;
18-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                    New mutein(s) of proteins - with fibroblast growth factor receptor activity, useful for treating multiple endocrine neoplasia, prostatic hypertrophy, used for diagnosis Example 3; Fig 8; 88pp; English.

A cDNA library prepared from human cancer cell line Kato III mRNA was screened with an oligonucleotide corresponding to amino acids 529-541 of chicken basic FGF receptor. Three positive clones were obtained. One was cloned into pUC118/119 to give pTR1228 (see 014848). The complete FGF coding sequence was obtained by ligating the insert from pTR1228 to the DNA sequence of the plasmid pTR128 insert which encodes the carboxyl terminus of the FGF receptor from the complete FGF coding sequence of the plasmid pTR1281 insert which encodes the carboxyl terminus of the FGF receptor from the complete FGF coding sequence of the plasmid pTR1281 consert which encodes the carboxyl terminus of the FGF receptor from the complete FGF coding sequence of the plasmid pTR1281 consert which encodes the carboxyl terminus of the FGF receptor from the formal property of the first plasmid pTR128 codes are conserved to the plasmid pTR128 codes are conserved to the plasmid pTR128 codes are codes as the carboxyl terminus of the FGF receptor from the first plasmid pTR128 codes are codes as the carboxyl terminus of the FGF receptor from the first plasmid pTR128 codes are codes as the carboxyl terminus of the FGF receptor from the first property of the first pr
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                                                                                                                                                                                                                                                                                                                                    Glu 533 c
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TAKE ) TAKEDA CHEMICAL IND KK. Igarashi K, Senoo M, Watanabe T; WPI; 91-353723/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clone pTB1283 encoding complete FGF receptuman; fibroblast growth factor; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; R15269.
New mutein(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9117183-A.
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Bollon AP, Torczynski RM;
                                                                                                                     289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               554 CAGGAGTTCCAGACCAGCCTGG 575
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les 22; Conserv
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uence 2310 BP;
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                                                                                                                     CAGGAGTTCCAGACCAGCCTGG
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                                                                                                                                                                                  . Similarity
22; Conserv
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25. .1983
/*tag= a
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Pred. No.
                                                                                                                                                                                                           Score 22;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                    566 C;
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0.023;
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0.024;
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T67164/c
ID T67164
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Q1485017
Q1485017
Q1016
Q10
PRESENTATION OF THE PRESEN
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14-NOV-1991.
25-APR-1991; J00557.
27-APR-1990; JP-113146.
31-JUL-1990; JP-204438.
14-SEP-1990; JP-245256.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New muterin(s) of proteins - with fibroblast growth factor receptor activity, useful for treating multiple endocrine neoplasia, prostatic hypertrophy, used for diagnosis Example 3; Fig 7; 88pp; English.

A cDNA library prepared from human cancer cell line Kato III mRNA a control with an oligonucleotide corresponding to amino acids 529-541 of chicken basic FGF receptor. Three positive clones were obtained. One was cloned into pUC118/119 to give pTB1229 (see 014849). The complete FGF coding sequence was obtained by ligating the insert from pTB1229 to the DNA sequence of the plasmid pTB1281 insert which encodes the carboxyl terminus of the FGF receptor from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q14850;
Q14850;
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                                                                                                                                                                                                                                                                        exon
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Homo sapiens.
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Sequence 2676 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human alpha-N-acetylglucosaminidase gene. Alpha-N-acetylglucosaminidase; mucopolysaccharidosis
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P-PSDB; R15268.
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(TAKE ) TAKEDA CHEMICAL IND
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990. .1372
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1373. .2114
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2115. .2262
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3203. .338
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1. .989
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Pred. No.
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(WOME-) WOMEN'S & CHILDREN'S HOSPITAL.

Anson DS, Blanch L, Hopwood JJ, Sco

WPI; 97-298114/27.

D-DERDS 170777
                                                                                                                                                                                                                                                                                                                                                                                                                      human alpha-N-acetylglucosaminidase (W18017), an enzyme that can hydrolyse the terminal alpha-N-acetylglucosamine residues at the non-reducing terminus of fragments of heparan sulphate and heparin. It was isolated by hybridisation of a human chromosome 17 library. A cDNA clone (T67163) coding for the enzyme has also been isolated. The isolated gene or cDNA, and primers/probes based on them or their complementary strands, can be used to investigate, diagnose and treat alpha-N-acetylglucosaminidase deficiency, for example in patients suffering from mucopolysaccharidosis type IIIB.

Administration is by oral, i.v., i.p., enzyme replacement therapy,
                                                                       exon
                                                                                                                       exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid encoding mammalian alpha-N-acetylglucosaminidase - used for the diagnosis and treatment of mucopolysaccharidosis type IIIB, also used in gene therapy Claim 8; Page 54-61; 79pp; English.
A genomic DNA molecule (T67164) includes 6 exons that code for A genomic DNA molecule (T67164) includes 6 exons that
                                                                                                                                                                              Clone of recombinant human kappa casein gene fragment. Casein; supplement; milk; pharmaceutical; ss.
                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                             Q46852 standard; DNA; 13104
                                                                                                                                                                                                                                                                                          7439 CAGGAGTTCCAGACCAGCCTGG 7418
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23-NOV-1995; AU-006
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0.025;
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T71699
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T71696
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10-JAN-1995; US-370975.
(HEAL-) HEALTH RES INC.
Maley F, Maley GR, Well; 97-244391/22.
T71696 standard; DNA; 26764
T71696;
20-AUG-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence encodes the human deoxycytidylate (dCMP) deaminase intron 2, which comprises 20303 base pairs from nucleotides 1964-22266 of the dCMP deaminase sense strand. The dCMP deaminase gene contains a 5' untranslated region (including the promoter), 5 exons, 4 introns and a 3' untranslated region (including the stop signals). The gene can be used to produce recombinant dCMP deaminase, which can be used to convert dCMP to dUMP. Also, the dCMP gene can be altered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding human deoxycytidylate deaminase recombinant deaminase Claim 2; Column 83-100; 58pp; English. The present sequence encodes the human deoxyc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T71by;
20-AUG-1997 (first entry)
Human deoxycytldylate deaminase
Human deoxycytldylate deaminase
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T71699;
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Sequence 13104 BP; 4256 A; 2497 C; 2397 G; 3953 T;
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25-JAN-1993; DK00024.
23-JAN-1992; DK-000088.
(SYMB-) SYMBICOM AB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (removed or mutated) to alter DNA replication
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                                                                                                                                                                                        CAGGAGTTCCAGACCAGCCTGG
                                                                                                                                                                                                                                                                                             Similarity
22; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                               20303 BP;
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                                                                                                                                                                                                                                                                                                                  6.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                            5454 A;
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                                                         ВР
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                                      V20441/c
                                                                                                                Query Match
Best Local Similarity
Matches 22; Conser
                                                                           17247 CAGGAGTTCCAGACCAGCCTGG 17268
                                                                                                                                                               Claim 3; Column 55-78; 58pp; English.

Claim 3; Column 55-78; 58pp; English.

The present sequence encodes the human deoxycytidylate (dCMP) deaminase gene, which contains a 5' untranslated region (including the stop signals). The gene can be used to produce recombinant dCMP deaminase, which can be used to convert dCMP to Also, the dCMP gene can be altered (removed or mutated) to alter replication in cells, which may lead to mutagenesis.

Sequence 26764 BP; 7079 A; 5521 C; 6539 G; 7625 T;
                                                                                                                                                                                                                                                                                     (HEAL-) HEALTH RES INC Maley F, Maley GR, WO WPI; 97-244391/22.
Human c-fms oncogene
                  V20441 standard; DNA; 35100
V20441;
                                                                                                                                                                                                                                                         DNA encoding human deoxycytidylate deaminase - recombinant deaminase
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10-JAN-1995;
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                                                                                              289 CAGGAGTTCCAGACCAGCCTGG 310
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                                                                                                                  Conservative
        (first entry)
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25392. .:
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23741. .:
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1. .1317
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1964. .22266
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*tag= f
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Pred. No.
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Best Local
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US5734039-A.
31-MAR-1998.
15-SEP-1994; 306691.
15-SEP-1994; US-306691.
(UYJE-) UNIV JEFFERSON THOMAS.
Calabretta B, Skorski T;
WPI; 98-229882/20.
human chromosome 10, 10q25.2 region. The sequence contains an unusual chromosomal marker referred to as mardel(10). The mardel(10) marker is mitotically stable and contains a functional neocentromere at a location regarded as non-centromeric. This neocentromere maps to q25.2 on chromosome 10. The specification describes nucleic acid sequences derived from a eukaryotic chromosome, including a neocentromere or its functional derivative or hybrid, that are able, in a compatible cell, of replicating, acting as extra-chromosomal element and segregating during cell division. The sequences can be used to construct artificial chromosomes for use in gene therapy comprising a replicable, segregating nucleic acid that confers a specific phenotype on cells. Human artificial chromosomes can propagate in human cells and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33551 CAGGAGTTCCAGACCAGCCTGG 33530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytoplasmic oncogene or proto-oncogene selected from ras, raf, EGF-1, c-fms, c-ros, c-kit, c-met, c-trk, c-src, c-abl, bcr-abl, c-fgr and c-yes. The second oligonucleotide is specific for a nuclear oncogene or proto-oncogene selected from myc, jun, c-ets, c-fos, c-myb, B-myb, c-rel, c-vav, c-ski, c-spi, cyclin Dl, PML/RAR alpha, AMLI/MTG8, E2A/prl and ALL-1/AF-4. The composition is used for treating cancer. The combination of antisense oligonucleotides has synergistically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 targetting cytoplasmic and nuclear oncogene(s)
Claim 1; Column 59-90; 92pp; English.
The present sequence represents an oncogene from the present invention describes a composition which comprises two antisense oligonucleotides. The first oligonucleotide is specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NC-contil derived from mardel(10) on chromosome 10q25.2.

Yeast artificial chromosome; YAC; probe; eukaryotic chromosome; neocentromere; replication; extra-chromosomal element; segregation; cell division; artificial chromosome; gene therapy; mardel(10); human artificial chromosome; transgenic; chromosome 10; 10q25.2; ss.
                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid comprising neocentromere sequences from eukaryotic chromosome - used to produce replicable, segregating artificial chromosomes that can carry large amounts of DNA for ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; oncogene; proto-oncogene; neoplastic disease; anticancer;
cancer; antisense oligonucleotide; c-fms; ds.
                                                                                                                                                                                                                                          The present sequence represents the NC-contig derived from a human chromosome 10, 10q25.2 region. The sequence contains
                                                                                                                                                                                                                                                                                      Claim 9; Fig 16A; 540pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                Cancilla MR, Choo K, WPI; 99-009773/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            enhanced ability to inhibit growth of cancer cells. Sequence 35100 BP; 8474 A; 8597 C; 9682 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anticancer composition comprising two anti-sense oligo:nucleotide(s)
                                                                                                                                                                                                                                                                                                                                                                                                                  (AMRA-) AMRAD OPERATIONS PTY LTD. Cancilla MR, Choo K, Du Sart D;
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13-MAY-1998; AU0352.
26-AUG-1997; AU-008791.
13-MAY-1997; AU-006791.
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03-MAR-1999
                                                                                                                                                                                                                                                                                                               therapy
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100.0%
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Pred. No.
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0.026;
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27312 CAGGAGTTCCAGACCAGCCTGG 27333
                                                                                                                                                                                                                                                                                                                                                                                                                             neccentromere at a location regarded as non-centromeric. This neccentromere maps to q25.2 on chromosome 10. The specification describes nucleic acid sequences derived from a eukaryotic chromosome, including a neccentromere or its functional derivative or hybrid, that are able, in a compatible cell, of replicating, acting as extra-chromosomal element and segregating during cell division. The sequences can be used to construct artificial chromosomes for use in gene therapy comprising a replicable, segregating nucleic acid that confers a specific phenotype on cells. Human artificial chromosomes can propagate in human cells and carry large amounts of DNA (e.g. therapeutic genes), and, being extra-chromosomal, they are not mutagenic. The artificial chromosomes are also useful for generation of transgenic plants and animals, in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               carry large amounts of DNA (e.g. therapeutic genes), and, being extra-chromosomal, they are not mutagenic. The artificial chromosomes are also useful for generation of transgenic plants and animals, in production of proteins and to make diagnostic reagents, e.g. for expression of cytokines, receptors and growth factors, or to increase the copy number of a gene in a cell. The constructs may also be used for functional and structural analysis of chromosomes. Sequence 80240 BP; 23102 A; 16537 C; 16747 G; 23846 T;
                                                                                                                                                                                                                                                                               production of proteins and to make diagnostic reagents, e.g. for expression of cytokines, receptors and growth factors, or to inc the copy number of a gene in a cell. The constructs may also be used for functional and structural analysis of chromosomes.

Sequence 80595 BP; 23183 A; 16613 C; 16824 G; 2397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-NOV-1998.
13-MAY-1998; AU0352.
26-AUG-1997; AU-006784.
13-MAY-1997; AU-006784.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yeast artificial chromosome; YAC; probe; eukaryotic chromosome; neocentromere; replication; extra-chromosomal element; segregation; cell division; artificial chromosome; gene therapy; mardel(10); human artificial chromosome; transgenic; chromosome 10; 10q25.2; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          eukaryotic chromosome - used to produce replicable, segregating artificial chromosomes that can carry large amounts of DNA for gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid comprising neocentromere sequences from eukaryotic chromosome - used to produce replicable, segregating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AMRA-) AMRAD OPERATIONS PTY LTD. Cancilla MR, Choo K, Du Sart D; WPI; 99-009773/01.
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WO9851790-A1.
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                                                              289 CAGGAGTTCCAGACCAGCCTGG
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                                                                                                                                                           Local Similarity
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                                                                                                                                 Conservative
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Pred. No.
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Pred. No.
                                                                                                                             Mismatches
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                                                                                                                                                           DB 1;
0.026;
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0.026;
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Search completed: October Job time: 7334 sec
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Sequence 158 HP; 46 A; 35 C; 44 G; 30 T;
                                                                                                                                                                 Query Match
Best Local Similarity
Matches 21; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection;
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
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35 C;
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Maximum DB seq length: 200000000
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1: gb_bal:*
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205
1 GCAAACAGAGCGCCACTGGG.....TACTTTGAAACATCTACTGG 205
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SUMMARIES

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ACU241// Homo sapi	6 Homo	AC011640 Homo sapi	AC011021 Homo sapi	AC008471 Homo sapi	AC021203 Homo sapi	Ното	AC023220 Homo sapi	Ното	Home	AC010429 Homo sapi	Z99572 Human DNA s	AL136089 Homo sapi	AC022747 Homo sapi	AL034563 S.pombe c	271781 S.cerevisia	274088 S.cerevisia	X15135 Yeast NAT 1	I09397 Sequence 5	I08122 Sequence 1	M23166 S.cerevisia	AL121928 Homo sapi	ij	U95626 Homo sapien		Description	

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REFERENCE
AUTHORS
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Regions
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Submitted (27-MAR-1997) Advanced Genome Sequence Analysis Course, Submitted (27-MAR-1997) Advanced Genome Rd., Cold Spring Harbor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      McComble, W.R., Wilson, R., Chen, E., Gibbs, R., Zuo, L., Johnson, D., Mhan, M., Parnell, L., Dedhia, N., Ansari, A., Mardis, E., Schutz, K., Gnoj, L., de la Bastide, M., Kaplan, N., Gerco, T., Touchman, J., Muzny, D., Chen, C.-N., Evans, C., FitzGerald, M., See, L.H., Tang, M., Porcel, B.M., Dragan, Y., Giacalone, J., Pae, A., Powell, E., Solinsky, K.A., DeSilva, U., Diaz-Perez, S., Zhou, X., Yu, Y., Watanabe, M., Doggett, N., Garcia, D. and Sagripanti, J.-L. Human BAC clone, 110P12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 143068)
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/db_xref="taxon:9606"
/chromosome="3"
                                                                                 Location/Qualifiers
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59206 63708 - 63998
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ccr2a (ccr2), ccr5 (ccr5) and ccr6
and lactoferrin (lactoferrin) gene,
                                                                                                                       53303 -
65200 -
112377 -
134914 -
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AF055992 Homo sapi
U4899 Human signa
S76830 glycoprotei
AE001168 Borrelia
AC014464 Drosophil
AF077546 Caenorhab
AP001049 Homo sapi
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X96440 E.chrysanth
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59531. 64785
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/gene="ccr5"
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/note="cr2"
/codon_start=1
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FYGMMLVILIILINCKKKMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQ
LUTGLYFIGFFSGIFFILLTIDRYLAVVHAVVALKARTVTFGVVTSVLTWVVAVFAS
LPGIIFTRSQKEGLHYTCSSHFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYSGIL
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LPPLYSLVFIFGFYGNMLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSA
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SVITMLVAVFASVPGIIFTKOQKEDSVYVCGPFPRGWNHHTIFHTHANLIGLVLPLIN
VICYSGILKTILRCRNEKKHHRAVRVIFTIMIVYFLFWTPYNIVILLNTIFGEFFGLSN
CESTSGLDQATQVTETLGMTHCCINPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPV
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VICYSGILKTLLRCNWEKKRHRAVRVIFTIMIYGFLFWIYNIVILLNTEGEFFGLIN
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CGSTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFHIALGCRIAPLQKFVCGG
PGVRPGKNVKYTTGGLLDGRGKGKSIGRAPEASLQDKEGA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="confirmed by similarity to Human monocyte chemoattractant protein 1 receptor (ccr2) mRNA (Accession Number U80924), two alternatively spliced mRNAs."
join(46106. .47046,48255. .48438)
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y GenBank Accession Number
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U54994."
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                                                                                                                                                                                            9.3%; Score 19;
Similarity 100.0%; Pred. No.
19; Conservative 0; Mismatch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_1d="aab57794.1"
/db_xref="G1:2104521"
/db_xref="G1:2104521"
/db_xref="G1:2104521"
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csavevigvlinluvvtlilvkxkglkrveniyillnlavsnlcfelflepwahaggdpm
criliclyfyglysffencllivqrklufliegelesdearrvpcgiitsvlawvtai
Latlefyvvykpomedqkykcafsrtpflpadeffwkheltlkmnisvluplpleifff
Lyvqnkktlrefedrysleklyfaimvyfllmaapyniafflsffkehfslsdcksy
Nldksyhitkiiatthccinpllyafldgtfskylcrcfhlrsntplqprgqsaqgts
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QAMQVTETLGMTHCCINPIIYAFVGEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPER
                                                                                                                                                                                                                                                                                                                 CAPGSDPRSNICALCIGDEQGENKCVPNSNERYYGYTGAFRCLAENAGDVAFVKDVTV
LQNTDGNNNDAWAKDLKLADFALLCLDGKRKPVTEARSCHLAMAPNHAVVSRMDKVER
LKQVLLHQQAKFGRNGSDCPDKFCLFQSETKNLLFNDNTECLARLHGKTTYEKYLGPQ
YVAGITNLKKCSTSPLLEACEFIKF
30122 c 32403 g 39349 t
                                                                                                                                                                                                                                                                                                                                                                                                               /translation="DLSDEAERDEYELLCPDNTRKPVDKFKDCHLARVPSHAVVARSV
NGKEDAIWHLLRQAOEKFGKDKSPKFQLFGSPSGQKDLLFKDSAIGFSRVPFRIDSGL
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TEDCIALVLKGEADAMSIDGGVYYTAGKCGLVPVLAENYKSQQSSDPDPNCVDRPVEG
YLAVAVVRRSDTSLTWNSVKGKKSCHTAVDRTAGWNIPMGLLFNQTGSCKFDEYFSQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="confirmed by similarity to lactoferrin mRNA, accession number M73700"
/product="lactoferrin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(join(124605 .124816,126528 .126717, 127884 .126068,130006 .130073,132033 .132164, 13863 .134018,135022 .135075,135890 .135980, 137445 .137599,138436 .138610,139077 .>139255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"confirmed by similarity to lactoferrin protein, encoded by GenBank Accession Number M73700, gi 186818"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(124782. .124816,126528. .126717, 127844. .126068,130006. .13073,13203. .132164, 13863. .134018,135022. .135075,135890. .13590, 13590, 137445. .137599,138436. .138610,139077. .>139253))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(124605. .>139255)
/gene="lactoferrin"
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Translated sequence exhibits 42% sequence identity to CCR5
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/product="ccr6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="lactoferrin"
/protein_id="AAB57795.1"
/db_xref="GI:2104522"
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)6642. .97676
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                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (22-JAN-2000) Lita Annenberg Hazen Genome Center, Col Spring Harbor Laboratories, 1, Bungtown Road, Cold Spring Harbo NY 11724, USA
On Mar 7, 2000 this sequence version replaced gi:6730690.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 16 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; Liliopsida; Poales;
                      Similarity
19; Conserv
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HTG; HTGS_PHASE1
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                                                                                                                                     /organism="Oryza sativa"
/db_xxef="taxon:4530"
/chromosome="10"
/clone="15522"
62170 a 45887 c 47331 g 6090
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                    9.3%; Score 19; DB
100.0%; Pred. No. 4.
tive 0; Mismatches
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    CTCTCTAATAAGAAAACAT 184
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AL121928
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Insert size: 164357; 5.4% error; agarose-fp
Quality coverage: 6.37x in Q20 bases; sum-of-contigs Quality
coverage: 8.57x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Assembly program: XGAP4; version 4.5 sequencing vector: M13; M77815; 15% of reads Sequencing vector: plasmid; L08752; 84% of reads Sequencing vector: plasmid; L08752; 84% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Consensus quality: 20342% bases at least Q30 Consensus quality: 215952 bases at least Q30 Consensus quality: 215972 bases at least Q30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (20-APR-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    On Apr 22, 2000 this sequence version replaced gi:7452949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens chromosome 10 clone RP11-18114, PROGRESS ***, in unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center project name: bA18I14
----- Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Informatio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center code:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Sanger Centre
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HTG; HTGS_PHASE1; HTGS_DRAFT
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(bases 1 to 225415)
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Eutheria; Primates;
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68973. .71980
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/db_xref-"taxon:9606"
/chromosome="10"
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fragment_chain:3"
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fragment_chain:2"
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fragment_chain:1"
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fragment_chain:1"
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fragment_chain:1"
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ragment_chain:2"
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185003. .186125
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213397. .21498
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187454. .188976
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fragment_chain:5"
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191994. .193218
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189077. .190281
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                                                                                                                                                                                                                                                2h 8.8%; Score 18; DB 7;

18; Similarity 100.0%; Pred. No. 27;

18; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                       Chromosome
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Molecular cloning and sequencing of a cDNA encoding N
alpha-acetyltransferase from Saccharomyces cerevisiae
J. Biol. Chem. 264 (21), 12339-12343 (1989)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Draft entry and computer-readable sequence [1] kindly submitted F.-J.Lee, 10-APR-1989.
    108122.1
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OPEDDQLDFHSYCMRKGTPRAYLEMLEMGKALYTKPMYCHAMKEASKLYPOMHDDRLK
RKSDSLJENSDBIQNNGONSSSOKKKAKKEAAAMNKRKETEAKSVAAYPSDQDNDVFG
EKLIFTSTPMEDFATTEFYNNYSMQVREDERDYILDFENYRIGKLALGFASLNGFAKR
FGTTSGLFGSMAIVLLHATRNDTPFDPILKKVYTKSLEKEYSENFPLNEISNNSFDWL
NFYQEKFGKNDINGLLETYRYENDDYPIGSSNLKEMIISSLSPHEPHSQNEILQYYL"
491 c 533 g 748 t
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HFLFLKDFPKAQEYIDAALDHTPTLVEFYILKARILKHLGLMDTAAGILEEGRQLDLQ
DRFINCKTVKYFLRANNIDKAVEVASLFTKNDDSVNGIKDLHLVEASWFIVEQAEAYY
GI:589163
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NWTSLAVAQDVNGERQQAINTLSQFEKLAEGKISDSEKEHSECLMYKNDIMYKAASD
NODKLQNVLKHLNDIEPCVFDKFGLLERKATIYMKLGQLKDASIVYRTLKRNFDDFK
YKKLLEVSIGIQGDNKLKKALYGKLEQFYPRCEPPKFIPLTFLQDKEELSKKLREYVL
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/strain="TD71.8"
/db_xref="taxon:4932"
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/protein_id="AAA88728.1"
/db_xref="GI:172028"
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\1LKKDGSHVDSLALKGLDLYSVGEKDDAASYVANAIRKIEGASASPICCHVLGIYMR
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                                                                             Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.
1 (bases 1 to 3347)
                                                                                                                                                           SCNAT 3347 bp DNA PLN
Yeast NAT 1 gene for N-terminal acetyltransferase.
X15135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5 from Patent 109397
                                 Direct Submission
Submitted (27-APR-1989)
Angeles CA 90024, USA
                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 2724)
Smith,J.A. and Lee,F-J.S.
Patent: Wo 8907138-A 5 10-AUG-1989;
Location/Qualifiers
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          Mullen, J.R.,
                                                                                                                                      acetyltransferase; NAT 1
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Smith, J.A. and Lee, F-J.S.
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                                                                  Grunstein, M
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Kayne, P.S., Moerschell, R.P., Colavito-Shepanski, M., Grunst
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                                             Grunstein M., UCLA, Biology Department,
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Sherman, F.
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Direct Submission
Submitted (09-JUL-1996) Data collected by MIPS on behalf of the Submitted (19-JUL-1996) Data collected by MIPS on behalf of the European yeast chromosome IV sequencing project. MIPS at the Max-Planck-Institut fuer Blochemie, Am Klopferspitz 18a D-82152 Martinsried, FRG; E-mail: Mewes@mips.embnet.org
Location/Qualifiers
1. .3530
                                                                                                                                                                                                                                                                                                                                            baker's yeast.
Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
                                                                                                                                                                                                                                       Saccharomycetaceae; Saccharomyces.

1 (bases 1 to 3530)

Paulin, L., Saren, A.M. and Laamanen, P. unpublished
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S.cerevisiae chromosome
274088 271256
274088.1 GI:1431024
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Identification and characterization of genes and w-+arminal acetyltransferase from yeast
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Location/Qualifiers
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EMBO J. 8 (7), 2067-2075 (1989)
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//db_xief="Swis-Prot: D12945"
//translation="MSRKRSTKREAKIALKENDOFLEALKLYEGROYKKSLKLLD
//translation="MSRKRSTKREAKIALKENDOFLEALKLYEGROYKKSLKLLD
AILKKDGSHVDSLALKGLDLYSVGEKDDAASYVANAIRKIEGASASPICCHVLGIYMR
AILKKDGSHVDSLALKGLDLYSVGEKDAASYVANAIRKIEGASASPICCHVLGIYMR
AILKKDGSHVDSTALKGLDLYSVGEKLAEGKISDSEXEHSECLMYKKVBAFLGYRA
NWTSLAVAODVNGEROOA INTLSQFEKLAEGKISDSEXEHSECLMYKKUDIMYKAASD
NQDKLQNVLKHLNDIEPCVFDKFGLLEKAATIYMKLGQLKDASIVYRTLIKRNPDNFK
YYKLLEVSLGIGGDNKLKKALYGKLEOFY PRCEPPKFIPLTFLODKEELSKLREVVL
POLERGVPANTESNVKPLYORRKSKVSPLLEKIVLDYLSGLDPTODPIPFIWNYYLSQ
HFLFLKDFPKAQEYIDAALDHTPTLVEFYILKARILKHLGLMDTAAGILEEGRQLDLY
DREINCKTVXYFLAANNIDKANTEVASLFTKNDDSVNGIKDLHLYGASWFTVQHADAYK
QFEDDQLDFFSYCMRGNTSSOKKAKKEDAAMNKRKETEAKSVAAYFSDQDINVFG
RKSDSLDENSDEIONNGOMSSSOKKKAKKEDAAMNKRKETEAKSVAAYFSDQDINVFG
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Eukaryota; Fungi; Ascomycota; Hemiascomycetes;
Saccharomycetaceae; Saccharomyces.
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act2 gene; actin; FAD synthetase; FAD1 gene; MPS1 gene; NAM1 gene;
NAT 1 gene; protein kinase; protein phosphatase; SIR2 gene; SIT4
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                                                                                         Submitted (23-APR-1996) Paulin L., Institute of Biotechnology, DNA sequencing & Synthesis Laboratory, Biocentre 1, P.O.BOX 56 (Viikinkaari 9), FIN-00014 University of Helsinki, Finland
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DRFINKTVKFFLRANNIDKAYEVASLETKNDDSVNGIKDLHLVEASWFIVEQAEAYY
DRFINKKKLDDLASLKKEVESBKSEQIADIKENGMUTAKKKKLDLALKRENNIPFRYK
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RKSDSLDENSDEIQNNGONSSSOKKKAKKEAAAANNKREFEAKSYAAYSSDODNDYFG
RKTISTERNWEDENSSSOKKKAKKEAAAANNKREFEAKSYAAYSSDODNDYFG
RKTISTERNWEDENSSSOKKKAKKEAAAANNKREFEAKSYAAYSSDODNDYFG
RKTISTERNWEDENSSSOKKKAKKEAAAANNKREFEAKSYAAYSSDODNDYFG
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FGTTSGLFGSMAIVLLHATRNDTPFDPILKKVVTKSLEKEYSENFPLNEISNNSFDWL
NFYQEKFGKNDINGLLFLYRYDDDVPIGSSNLKEMIISSLSPLEPHSQNEILQYYL"
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/gene="NAT1"
/db_xref="SGD:S0002198
                                               1. .36687
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/db_xref="GI:1431025"
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/db_xref="SGD:S0002198"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Saccharomyces cerevisiae"
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/strain="alpha S288c"
                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="unknown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(5030. .5950)
                                                                                                                                                                                                                       complement(6581. .7630)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LSQTFDLCETLEDNDIEGLSCPIEPGEYNIKKIVEIPGEVPPGKYVVVARAYTEKDDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="SIT4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard_name="D2717"
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                                                                                                                                                                                                                                                                                                    ement(11215. .13779)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'unknown"
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DEFINITION
ACCESSION
VERSION
KEYWORDS
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Best Local S
Matches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fission yeast.
Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales.
Schizosaccharomycetaceae; Schizosaccharomyces.
1 (bases 1 to 43325)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6-phosphogluconate dehydrogenase decarboxylating; cell wall protein; class v pyridoxal phosphate dependent aminotransferase; elongation factor g; elongation factor Tu family; fbpl; fructose-1,6-bisphosphatase; 6 beta repeat; glycine-rich protein; low-complexity gene-free region; mikl; mitosis inhibitor protein kinase mikl; myb like dna-binding protein; neutral trebalase; ntpl; polya-binding protein; rasll; replication factor-a protein 1; polya-binding protein; RNA recognition; RNA3' Cleavage factor Ib; rpal; ssbl; transcription initiation factor iif beta subunit; WD domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18;
                                                                                                                                                                                                                                                                                                          sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 15A, E-mail: barrell@sanger.ac.uk and Biotechnologische und molekularbiologische Forschung, angelhofweg 39, D-69259 Wilhelmsfeld, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                               Lyne,M., Rajandream,M.A., Barrell,B.G. and Rieger,M. Direct Submission Submitted (18-DEC-1998) European Schizosaccharomyces
Commission. Fourteen European sequencing laboratories, the Sanger Centre, are participating in the project. Protein coding regions (CDS) have been predicted with
                                                                                           (URL, http://www.sanger.ac.uk/Projects/S_pombe/)
During 1995 to 1996 about 66% of S. pombe chromosome
sequenced by the Sanger Centre. The sequencing of th
genome is now being continued with funding from The E
                                                                                                                                                                                                               Details of yeast sequencing at the Sanger Centre are the World Wide Web.
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YYKLLEVSLGIQGDNKKKALYGKLEQFYPCEPFKFIFLTFIQDKEELSKKLREYVL
PQLERCVPATFSNVKPLYQRRKSKYSPLLEKIYLDYLGGLDPTQDDIPFTWNYYLLSQ
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RKSDSLDENSDEIQNNGQNSSGKKRAKEAAAMNKRKETETEAKSVAAYPSDQDNUVFG
EKLIETSTPMEDFATEFYNNYSMGVPEDERDYILDFEFWRIGKLALCFASLNKFAKR
FGTTSGLFGSMAIVLHATRNDTPFDPILKKVVTKSLEKEYSENFPLNEISNNSFDWL
NFYQEKFGKNDINGLLFLYRYRDDVPIGSSNLKEMIISSLSPLEPHSQNEILQXYL"
complement(14327...14674)
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/db_xref="GA96457"
/db_xref="SPTREMBL:Q12459"
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/db_xref="SWISS-PROT:P12945"
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%; Pred. No. 19;
0; Mismatches
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. 19;
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IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.

Cosmid c660 is overlapped at the 3' end by cosmid 1198 (contained in EMBL entry SP33010 accession number U33010).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           splice donor/acceptor sites.

CDS are numbered using the following system eg pombe), B (chromosome 2), c25H2 (cosmid name),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        computer analysis using the Genefinder program in PomBase (an ACED) database) with additional predictions for the branch-acceptor sites supplied by the program $93$plice. CAUTION: It is possible that for any individual CDS we may have underestimated or overestimated the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     number of introns/exons or we may not have chosen the correct
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/note="SPBC660.01c, SIMILARITY:Schizosaccharomyces pombe, CAB52717, putative myb-like dna-binding protein,, (496 aa), fasta scores: opt: 478, E():4.7e-23, (30.6% identity in 350 aa)"
                                                                                                                                                                                                                                                                                                                                                           /note-"gtaagt, splice donor sequence" complement(join(383..464,506..537))
/gene-"SPBC660.01c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pombe chromosome 2" complement(87. .104) /gene="SPBC660.01c"
                                                                                                                                                   /note="ttaacgtttag, splice branch and acceptor"
complement(500..505)
/gene="SPBC660.01c"
                                                                                                                                                                                                                                                                /note="Match to PF00249 myb_DNA-binding, Myb-like DNA-binding domain Score 30.86" complement(465. .475)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="ctaatattttaattttaag, splice branch
complement(132, .137)
/gene="SPBC660.01c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WDYLERRMONECOTYSLDHTQVADSLHEKRLHGPLSSLVKLLVGEMPSTTRRTLIRHL
RALYNIPGYEKYSRKNSSGGGDYQETA, II SOEVHNET INGGWSEYJGFCNQIWAGKC
PKTIZMFYSULYKKLSHDAKSIYHHVRRAYNPFEDRCVWSKEEDEELKKVVUEHGKC
WTKIGRKMARMPNDCRDRWRDVVRFGDKLKRNAWSLEEETQLLQIVAELRNREDLSSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MDTSVLNPELQIHGFIGVDSLQSSRKRKNDFDDFFLNKGLKTNN
NDYSGSIEPKFSPALSIKEDGKNDRNFEALMSLQAQDSNLSEQNTSIHLDALASSSIA
LGNDNVDSSAFLSKVNKGVNAMRNSTSNQTNDSILISPSEITNMDPFLKGSARWTAEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INWTLVAQMEGTRTRLQCRYKFQQLTKAASKFELQENVWLLERIYDSLLNNGGKIHWE
NIVKEANGRWTRD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="putative myb like dna-binding protein"
/protein_id="CAA22521.1"
/db_xref="GI:4049500"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="nominal overlap with cosmids
pombe chromosome 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label-SPBC660.01c
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/gene="SPBC660.01c"
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/strain="972h-"
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                                                                 /gene="SPBC660.02"
618. .2738,2785. .3929)
"SPBC660.02"
                                                                                                                   tatgt, splice donor sequence"
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/gene="$BEC660.02"
/note="Match to PF00400 WD40, W
Score 31.68"
3771. 3884
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/gene="SPBC660.03c"
/note="SPBC660.03c, len:307, SIMILARITY:Saccharomyces
cerev isiae, YGR005C, TZFB_YEAST, transcription initiation
factor iif, beta subunit, (400 aa), fasta scores: opt:
461, E():2.9e-32, (31.0% identity in 368 aa);
SPBC660.03c, len:307, SIMILARITY:Saccharomyces cerevisiae,
TZFB_YEAST, transcription initiation factor iif, beta
subunit, (400 aa), fasta scores: opt: 461, E():1.4e-22,
(31.0% identity in 368 aa)"
                        /note="ctaacttttttttcag,
complement(4485..4490)
/gene="SPBC660.03c"
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GSQVCNMAWSKTSNEIVTTHGFAKNQVSLWKYPSLKNIANLTAHTNRVLYLSMSPDGQ
SIVTGAGDETLRFWKLFNKKPKEESTLIR"
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fmellsmelfgsqasrsrafyygedkrkiekkmldtpdrksyslspispqsqdmlrqp
qkpkrafpktpykildapylkndfylnlldmgqsnvlavglassiylmsaasgkvvql
                                                                                                                              /note="gtatgt, splice donor
complement(4432...4447)
                                                                                                                                                                                                         /note-"ctaatgaattcatattag, complement(4282. .4287)
                                                                                                                                                                                                                                                                                                                  VKQPEVYLKEVLDSIAILNKRGPYALKYSLKPEYKGTMDAASVELRNQQASQSESSSI
DHTGKNTSPDNPGTNAEEDEDDDGVEMIDVV"
                                                                                                                                                                                                                                                                                                                                                                   /translation="MSEEKPTVRTEEDDRYEDDAGDLDLGQIGSRVWLVKIPKFIMDK
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TSSSMKSTALVGTVAHECNVSPVINDDYRRVMQKRALASAPKRKVQMLDDRGGSLA
PGTLGSRSRSTTSFIRNVKPRTGEGLKNSRIPRNELLDILFKCFEDYEYWTLKGLREY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="gtatgt, splice donor sequence"
2772. .2784
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NTLTSGGKDEVILHHDLRAPGCCAEMMKVHEQEICGLQWDRSLGQLASGGNDNNLFVW
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pombe, 013286, srw1., (556 aa), fasta scores: opt: 1364,
E():0, (50.6% identity in 385 aa)"
                                                                                                                                                       /gene="SPBC660.03c"
/note="graff"
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score 20.22"
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/note="Match to PF00400 WD40, WD domain, G-beta repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="SPBC660.02"
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/product="transcription initiation factor iif, beta
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                                                                                                        'gene="SPBC660.03c"
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splice donor sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 83536)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 4, clone RP11-131K9
                                                                                                                                                 Direct Submission
Submitted (06-FEB-2000) Whitehead Institute/MIT Center
                                                                                   http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Birren, B., Linton,
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/product="fructose-1,6-bisphosphatase"
/protein_id="cna22524.1"
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* sequencing reads that have not been assembled into

* contigs. Runs of N are used to separate the reads

* and the order in which they appear is completely

* arbitrary. Low-pass sequence sampling is useful for

* identifying clones that may be gene-rich and allows

* overlap relationships among clones to be deduced.

* However, it should not be assumed that this clone

* will be sequenced to completion. In the event that

the record is updated, the accession number will
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AL136089
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                                                                                                                                                                                                                                                                                        on Apr 9, 2000 this sequence version replaced gi:7320935.

IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage etc. Order of segments is not known; 800 n's separate beginners. Contig_ID: 00643 Length: 7735bp Contig_ID: 00773 Length: 17572bp Contig_ID: 00773 Length: 17572bp Contig_ID: 00923 Length: 76087bp.

* NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        requests:
On Apr 9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AL136089 102995 bp DNA HTG
Homo sapiens chromosome 6 clone RP1-278E11,
PROGRESS ***, 3 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (08-APR-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
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26109 26508: gap of 800 bp
26909 102995: contig of 76087 bp in length
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                                         /clone="RP1-278E11"
/clone_lib="RPCI-1"
                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
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                                                                                                                                                                                                                                                                                                                                                                                     The true right end of clone 206D15 is at 104.
The true right end of clone 86F14 is at 10651.
86F14 is from the library RPCII constructed at the Roswell Park
Cancer Institute by the group of Pieter de Jong.
For further details see http://bacpac.med.buffalo.edu/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              only a small overlap as described above.

This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre chromosome 1 mapping group. Further information can be found at http://www.sanger.ac.uk/HGP/Chrl/

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neighbouring submissions.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variations annotated may not be found in the sequence submission corresponding to the overlapping clone as we submit sequences with only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (13-JAN-1998) Chromosome 1 Project Group (http://www.sanger.ac.uk/HGP/Chr1/) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquires: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Jan 13, 1998 this sequence version replaced gi:2578147.
IMPORTANT: This sequence is not the entire insert of clone 86F14. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
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Human DNA sequence from
coagulation factor V, ES
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1 (bases 1 to 106571)
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/clone="RP1-86F14"
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                                                                                                                                                                                  .302 of
                                                                                                 .323 of consensus"
                     .1 of
                                                           .568 of consensus"
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                   consensus *
                                                                                                                                                                                    consensus"
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/note="rLIMA7 repeat: matches 1017. .895 of consensus"
/note="natch: multiple ESTs; match: R71060 H69028 R82016
/note="match: multiple ESTs; match: R71060 H69028 R82016
/note="match: multiple ESTs; match: R71060 H69028 R82016
/note="match: w03874 H74282 D85329"
complement()0in(27431. .27577,28562. .28744,31530. .31681,
33638. .33782.36315. .36470.36919. .37022,37955. .38026,
39019. .39135,41033. .41212,42726. .42936,43904. .44140,
49624. .49798,53412. .56232,57414. .57656,59560. .59710,
49624. .69983,72271. .72414,73672. .73884,85339. .85461,
99549. .95640,99347. .99504))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <25068. .25543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="LiPA6 repeat: matches 1. .890 of consensus" 22732 . .2827 / ... .2827 / ... .2827 / ... .2827 / ... .2825 / ... .2825 / ... .2851 / ... .2851 / ... .2851 / ... .2851 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 / ... .2852 /
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/note="MIR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="AluSc repeat: 3877 4060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="MIR repeat: matches complement(10749. .11106) /note="match: STS G05144" 11725. .12081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="L1 repeat: matches 5390.
2854. .3352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25302. .25381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="L1 repeat: matches 3338.
19683. .20571
                              /db_xref="SPTREMBL:043737"
/translation="MFPGCPRLWVLVVLGTSWVGWGSQGTEAAQLRQFYVAAQGISWS
/RPEPTNSSLNLSVTSFKKIVYREYEPYFKKEKPQSTISGLLGPTLYAEVGDIIKVHF
                                                                                                                                                   /protein_id="CAB16748.1"
/db_xref="GI:2769647"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="MER45 repeat: matches 1. .178 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note-"MIR repeat: matches 49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="match: H61071 H69565"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="AluSq repeat: matches 303. .1 of consensus"
| 13253. .13367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note-"THE1C repeat: matches 371. .1 of consensus"
|2196. .12497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note-"AluY repeat: matches incomplete repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="L1MC2 repeat: matches 193. .10 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="L1ME1 repeat:
NKADKPLSIHPQGIRYSKLSEGASYLDHTFPAEKMDDAVAPGREYTYEWSISEDSGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note-"MLT1F repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="L1PA2 repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note-"L1 repeat: matches 4910.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="Alusc repeat: matches 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note-"MER20 repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="L1ME2 repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Ll repeat: matches 2971. .2759 of consensus" .26378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "MIR2 repeat: matches 4. .127 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Ll repeat: matches 2577.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .26062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .19825
                                                                                                                                                                                                                                                  actor V"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat: matches 22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   matches 18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         matches 570. .170 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            matches 687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .131 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .5390 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .4940 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .145 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .890 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .891 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .218 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .5194 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .5390 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .299 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .299 of consensus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  295 of consensus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .138 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .170 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        consensus"
```

Query Match
Best Local Similarity
Matches 18; Conserv repeat_region Conservative DVRTNINSSRDPDNIAAWYLRSNNGNRRNYYIAAEEISWDYSEFVQRETDIEDSDDIP
EDTTYKKVVFRKYLDSTFYKRDPRGEYEBHLGILGFIIRAFDDVIQVRRKNLASRPY
SLHAHGLSYEKSSEKYTEDDSPEWFKEDNAVQDNSSTYTYWHATERSGESGSGCFI
SLHAHGLSYEKSSEKYTEDDSPEWFKEDNAVQDNSSTYTYWHATERSGESGSGCFI
AWAYYSAVNPEKDIHSGLIGPLLICQKGIILHKDSNMPMDMREFVLLFMTFDEKKSWYY
EKKSKSSWRLTSSEMKKSHEFHAINGMIYSLFGLKWYEDGWVRLHILNIGGSQDIHVV
HEHGQTILLENGNQHQLGVWPFLLPSGFKTLENKASKPEWHLLNIEUGSKORAGNGYPEN
LIMDRDCKHPMGLSTGIISDSQIKASEFLGYWEEPRLARLNNGSYNAWSVEKLAAEFA
SKPWIQVDMOKEVIITGIOTQGAKHYLKSCYTTEFYVAYSSNQJUMQIFKGNSTRNVM
YFNGNSDASTIKENQFDPFIVARYIKISPTRAVIRPTLKELGGCEVNGCSTPLKMEN
GKIENKQITASSFKKSWMGDYWEFFRARLNAQGRVNAWQAKANNNKQWLEIDLLKIKK
GKHINGOLSGSEMYVKSYTHYSDGOVEWRYRLKSSMVDKIFEGNTNTKGHVKN
TPAIITGGCKSLSSEMYVKSYTHYSDGOVEWRYRLKSSMVDKIFEGNTNTKGHVKN ISPQNASRAWGESTPLANKPGKOSGHPKFPRVRHKSLQVRQDGGKŠRLKKSQFLIKTR
KKKKEHTHHAPLSPRTFHPLASEAYNTFSERRLKHSLVLHKSMETSLDTDLNQTLPS
MDFGMIASLPDHNQNSSNDTGQASCPPGLYGTPPEEHQQTVIFPDDDDQMHSTSDPSH
RSSSPELSEMLEYDRSHKSFPTDISQNSPSSEHEVWQTVISPDLSQVTLSPELSQTNLS
SPDLSHTTLSPELIQRNLSPALGQMPISPDLSHTTLSDLSQTNLSPEL
SQTNLSPALIQWPLSPDLSHTTLSLDESQTNLSPELSQTNLSPELSQTNLSPELIQRNESPELSQTNLSPELIQRNESPELSQTNLSPELIGNESPELSGTNLSPELSGTNLSPELSGTNLSPELSGTNLSPELIGNESPENGGWSLSPDLSQTN
SPTLNTTLSLDESQTNLSPELSGTNLSPELIGHTLSPDLSQTNLSPE
LSQTNLSPDLSHTTLSLDESQTNLSPELSGTNLSPELIGHTSPEL CENPDEVKRDDPKFYESNIMSTINGTVPËSITTLGFCFDDTVQMHFCSVGTQNEILTI
HTTGHSTIYGKEHEDTLYLFPMAGESVTVTTMDNVGTWMLTSMNSSPRSKLLKFRDV
KCIPDDEDSYELFEPPESTVAATRKMIDLLEPEDEESDADYDVQNLAAALGIRSFR
KSSLNQEEEFNLTALALENGTEFVSSNTDIIVGSNYSSPSNISKFTVNNLAEPOKAP
SHQQATTAGSPLAHLIGKNSVLNSSTAEHSSPYSBDIEDPLQDDVTGIRLLSLGAGE
FKSQEHAKHKOFKVERDOAAKHRFSWMKILAHKYGRHLSQDTGSPSGMRFWEDLDFQD
TGSPSRMRPWKDPPSDLLLLKQSNSSKILVGRWHLASEKGSYELIQDTDEDTAVNNWL /note-"MIR repeat: matches 104. .17 of consensus" 34738. .35036 /note-"Alusc repeat: matches 299. .1 of consensus 35051. .35542 FFNPPIISRFIRVIPKTWNQSIALRLELFGCDIY"
27629. .27788
/note="AluJo repeat: matches 302. .140 of consensus;
incomplete repeat" NLKKITREQRRHMKRWEYFIAAEEVIWDYAPVIPANMDKKYRSQHLDNFSNQIGKHYK KVMYTQYEDESFTKHTVNPNMKEDGILGPIIRAQVRDTLKIVFKNMASRPYSIYPHGV DESKSWSQSSSLMYTVNGYVNGTMPDITVCAHDHISWHLLGMSSGPELFSIHFNGQVL EQNHHKVSAITLVSATSTTANMTVGPEGKWIISSLTPKHLQAGMQAYIDIKNCPKKTR /note="MIR2 repeat: matches 103. .146 of consensus"
31903. .31988 THDDPPCLTHIYYSHENLIEDFNSGLIGPLLICKKGTLTEGGTQKTFDKQIVLLFAVF 46627. .46980 /note="L1MA7 repeat: matches 2. .364 of consensus" 46983. .47446 /note="L1 repeat: matches 3613. .5390 of consensus" 46627. .46980 /note="LlMA8 repeat: matches 1038. .944 of consensus" 44951. .46774 /note="MIR2 repeat: matches 146. .93 of consensus" 43456. .43548 /note="MADE1 repeat: matches 1. .53 of consensus"
43274. .43327 /note="MIR repeat: matches 75. .259 of consensus"
29041. .29084 28002. note="L1 repeat: matches 3215. .3729 of consensus" 8.8%; Score 18; DB 100.0%; Pred. No. 17; 0 Mismatches 10; •0 Length 106571; 👺 .1 of consensus" Indels , 0; . Gaps 0

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1250 TAATAAGAAAACATCTAC 1233

171 TAATAAGAAAACATCTAC 188

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JOURNAL
REFERENCE
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JOURNAL
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Matches 18
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                                                                                                                                                                                                                                     178 AAAACATCTACTTTGAAA 195
Homo sapiens chromosome 11 clone CMB9-21K9 map 11q22, WORKING SEQUENCE, 25 unordered pieces.

APO00817
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AC010429.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www.jgi.doe.gov
-----Summary Statistics
Consensus quality: 132291 bases at least Q40
Consensus quality: 133603 bases at least Q30
Consensus quality: 133603 bases at least Q20
Estimated insert size: 133783; sum-of-contigs estimation
Estimated insert size: 233000; pulse field gel estimation
Quality coverage: 4.87x in Q20 bases; pulse field gel estimation
Quality coverage: 8.48x in Q20 bases; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                              ch 8.8%; Score 18; DB 72; Length 133783; Similarity 100.0%; Pred. No. 16; 18; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Apr 5, 2000 this sequence version replaced g1:7212886.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 13783)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----Genome Center
Center: Joint Genome Institute
Center Code: JGI
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DOE Joint Genome Institute.
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HTG; HTGS_PHASE1; HTGS_DRAFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                         43496 a
                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/chromosome="5"
/clone="CTD-2199L14"
25289 c 24707 g 40291 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location,
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                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: This is a 'working draft' sequence. It currently consists of 25 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (03-DEC-1999) to the DDBJ/EMBL/GenBank databases. Masahira Hattori, The Institute of Physical and Chemical Reseau (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens DNA, clone:CMB9-21K9.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9924)
On Feb 19, 2000 this sequence version replaced g1:6997652.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hor
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujlyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo sapiens 139,740 genomic DNA of 1122
Published Only in DataBase (1999) In press
2 (bases 1 to 139740)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APO00817.2 GI:7007459
HTG; HTGS_PHASE1; HTGS
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1 (bases 1 to 139740)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://hgp.gsc.RIKEN.go.jp/
Contact: hattori@gsc.RIKEN.go.jp
Contect: project Information
Center project name: HumDraft11
Center clone name: CMB9-21K9

Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of re
Assembly program: Phrap; version 0.990329
Consensus quality: 112677 bases at least Q40
Consensus quality: 125720 bases at least Q20
Insert size: 129024; sum-of-contigs
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Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                113791 114290: gap of 500 bp in 14290: gap of 500 bp in 14291: gap of 502 bp in 1837 121836: gap of 502 bp in 1837 125424: contig of 3588 bp in 18425 125924: gap of 500 bp in 1845 125924: gap of 500 bp in 1845 125924: gap of 2107 bp in 1847 130196: contig of 1650 bp in 184274: contig of 1650 bp in 184274: contig of 1899 bp in 18478: gap of 134778: gap of 500 bp in 18478: gap of 1850 bp in 18478: gap of 1
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56603 57107: gap
65754:
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87385 87886; gap of
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47035 56602: contig of
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1867 77672: contig of 7673 78174: gap of 5
81813: contig of
                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                          ocation/Qualifiers
                                                                                                                                                                                   clone="CMB9-21K9"
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2762: gap of 50
97056: contig of 4
8.8%;
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7367: gap of 506 bp
09928: contig of 2561 bp
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71355: contig of
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33: gap of 500 bp
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ap of 510 bp
contig of 4681 bp in
conf 513 bp
4101 bp i
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Score 18;
Pred. No.
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f 5071 h
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Matches

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Mismatches

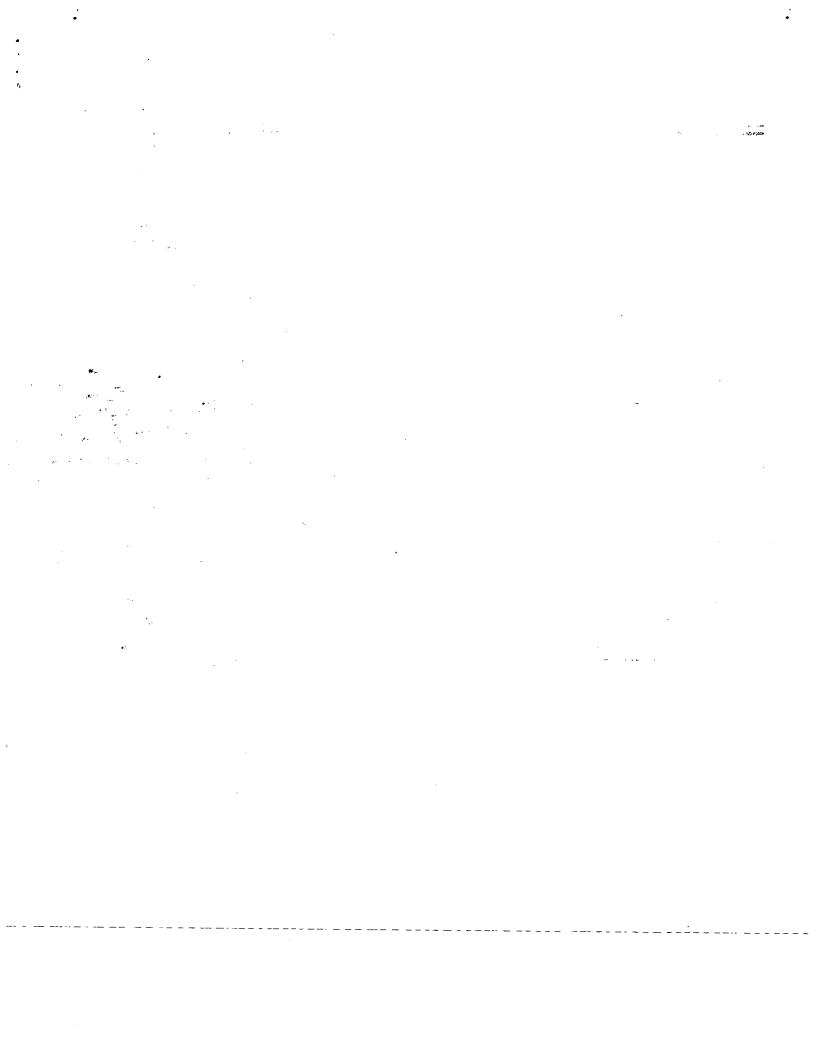
0;

Indels

Gaps

0;

Search completed: October 3, 2000, 12:59:51 Job time: 9393 sec



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Title:
Perfect score:
Sequence:
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Maximum DB
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214
1 CTAAGGCGTGCAAA
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Gapop 60.0 , Gapext 60.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Copyright
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gb_htg1: *
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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AC022414
AP001792
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AC018744
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U95626 Homo sapien
ACOL18744 Oryza sat
M23166 S.cerevisia
I08122 Sequence 1
I09397 Sequence 5
X15135 Yeast NAT 1
Z74088 S.cerevisia
ACOL1747 Homo sapi
ACOL1747 Homo sapi
ACOL2747 Homo sapi
ACOL2747 Homo sapi
ACOL2741 Homo sapi
ACOL2741 Homo sapi
ACOL2741 Homo sapi
ACOL2741 Homo sapi
ACOL1021 Homo sapi
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FEATURES Source		COMMENT	TITLE JOURNAL		NO THOMA	REFERENCE			REFERENCE	ORGANISM	VERSION KEYWORDS	• OBSTREETON	RESULT 1 HSU95626/c LOCUS			C 42		ი აკე აგ	c 34 35	332+		c c 27	N N M U	
143046 - 144068. Location/Qualifiers 1. 143068 /organism-"Homo sapiens" /db_xref-"taxon:9606" /chromosome="3"	31434 - 31443 37900 - 37968 53303 - 59166 - 59206 63708 - 63998 65300 - 78605 - 78713 92135 - 92137 112377 - 112643 - 112778 134284 - 134309 134914 -	erage are	Direct Submission Submitted (27-MAR-1997) Advanced Genome Some Cold Spring Harbor Laboratory, 1Bungtown I	Porcel, B.M., Dragan, Y., Giacalone, J., Pae, Solinsky, K.A., DeSilva, U., Diaz-Perez, S., Watanabe, M., Doggett, N., Garcia, D. and Sao	Nhan,M., Parnell,L., Dedhia,N., Ansari,A., Mardis,E., Sci. Gnoj,L., de la Bastide,M., Kaplan,N., Greco,T., Touchman Muzny,D., Chen,CN., Evans,C., FitzGerald,M., See,L.H.,	Human BAC cione 110P12 Unpublished (1997) 2 (bases 1 to 143068) WGCmbia D W William D Chan E Gibbs 1	Porcel, B.M., Dragan, Y., Giacalone, J., Pae, A., Powell, E., Solinsky, K.A., DeSilva, U., Diaz-Perez, S., Zhou, X., Yu, Y., Watanabe, M., Doggett, N., Garcia, D. and Sagripanti, JL.	Nhan,M., Parnell,L., Dedhia,N., Ansari,A., Gnoj,L., de la Bastide,M., Kaplan,N., Greco Muzny,D., Chen,CN., Evans,C., FitzGerald,	to 143068)	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata;			HSU95626 143068 bp DNA	ALIGNMENTS	7.9 39752 9 7.9 40677 50	7.9 23332 7.9 23379	.9 3068 10 .9 13271 2	7.9 2489 9 7.9 2772 11 7.9 2795 11	7.9 1850 1 7.9 2415 9	7.9 1155 39 7.9 1795 9	.4 240327 .4 260270	8.4 195832 78 8.4 216215 10	8.4 182482 43 8 4 186243 53	
	53357 65335 112551 135019	75:	Sequence Analysis Course, n Rd., Cold Spring Harbor,	•	, Mardis,E., Schutz,K., co,T., Touchman,J., l,M., See,L.H., Tang,M.,			, Mardis, E., Schutz, K., Do, T., Touchman, J., J.M., See, L.H., Tang, M.,	Zijo T.	Ħ		in (lactoferrin) gene,	PRI 16-MAY-1997		APULU4Y HOMO SEPI D86993 Homo sepien AC000099 Cosmid g0	AF077546 Caenorhab	S76830 glycoprote1 AE001168 Borrelia	X85785 H.sapiens D AF055992 Homo sapi U43899 Human signa	X96440 E.chrysanth AK001422 Homo sapi	AF100634 Homo sapi Y14873 Homo sapien	AC022422 Homo sapi AL135840 Homo sapi G61963 SHGC-89514	AC019184 Homo Sapi AL080239 Human DNA	AC016703 Homo sapi	
		CDS	gene		mRNA					CDS					CDS		gene		:	mRNA		,	BONA	
/protein_id="aab57793.1" /db_xref="gi:2104520" /db_xref="gi:2104520" /db_xref="gi:2104520" /db_xref="mdivyseptydinyytsepcokinykoiaarllpdlyslvfifg /translation="mdkovsspiydinylseptydecokinykoiaaakakakakakakakakakakakakakakakakaka	/note="confirmed by similarity to numan CC chemokine receptor 5 (ccr5) protein, encoded by GenBank Access Number U54994, g1 1457946" /codon_start=1 /product="ccr5"	6148362541 /gene="ccr5"	/product="ccr5" 5953164785 /gene="ccr5"	<pre>/gene="ccr5" /note="confirmed by similarity to receptor 5 (ccr5) mRNA. Accession</pre>	PACES OF LIBERTAIN CONTRACTORY OF THE TABLE	LPPLYSLVF I FGF VONMLVVLILLINCK ANEWVFGNAMCKLFTGLYHIGYFGGI FF SVITWLYAVFASVPGI I FTRCQKEDSVY VICYGGI KTI I FORMEWFBURA NEWIFF	/protein_id="AAB57792.1" /db_xref="GI:2104519" /translation="MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQL	Number: 1168965" /codon_start=1 /product="ccr2b"	<pre>/gene="ccrz" /note="confirmed by similarity to] chemoattractant protein 1 recentor</pre>	CESISQUIQAIVIELIAMINCCLNFILL PGVRPGKNVKVTTQGLLDGRGKGKSIGRA 4610647188	AREMY FIGHANCA DE TIGLIE IN LILILIDRI LAAV HAY YEALAKAKI Y LE GYY L SVITWILVAVFASYPGI IFT KCQKEDSYVCGGY YEFRGWNEHT IMKNI IGIVILLILLIL VICYSGILKTILTEGEN KKRHRAVRVI FT IMI VYFILWITYI ILICODA ANI GEDUCCO	/W_ALEL- GLIGADAO /translation-#ML5TSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQL LPPLYSLVFIFGFVGNYLVYLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSA	/codon_start=1 /product="ccr2a" /protein_id="AAB57791.1" /ib====================================	//octe-"confirmed by similarity to Human mono //octe-"confirmed by similarity to Human mono chemoattractant protein 1 receptor (ccr2) al- spliced A-form, Encoded by GenBank Accession U80924, gl 1168965"	Chemoartractant protein i receptor (CCF2) mxna (ACCESSION Number U80924), two alternatively spliced mRNAs." join(46106. 47046,4825548438)	/gene="ccr2" /note="confirmed by similarit	/product="ccr2a" 4605649505	chemoattractant protein 1 receptor (ccr2) alternatively spliced mRNA encoding A-form carboxyl tail, Accession Number U80924 "	/gene="ccr2" /note="confirmed by similarity to Human	/product = "cor25" /product = "cor25" /product = "cor25" / product	chemoattractant protein 1 receptor (ccr2) alternatively spliced mRNA encoding B-form carboxyl tail. Accession Number: fr8024."	/gene="ccr2" /note="confirmed by similarity	/clone="BAC 110P12"	

mRNA

Sg gene

Harbor,

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BASE COUNT
ORIGIN
 DEFINITION
                                                                                                                                                                                            Query Match
Best Local :
                                                                                                        32691 CTGGTCCCCACCTTTGCAG 32673
                                                                                                                      82 CIGGICCCCACCITIGCAG 100
AC018744 216514 bp
Oryza sativa chromosome
                                                                                                                                                                           19;
                                                                                                                                                                                            Similarity 100.0%;
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YLGSGYFTAIQNLRKSEEVAARRAKVWCAVGEQELRKCNQWSGLSEGSVTCSSAST
TEDCIALVLKGEADAMSLDGGYVTTAGKCGLVPVLAENYKSQQSSDPDPUCGSPVEGYLAVAVVRSDTSLTWNSVKGKKSCHTAVDRTAGWNIPMGLLENQTGSCKEDEYFSQS
CAPGSDPRSNLCALCIGDEQGENKCVPNSNERYYGYTGAFRCLAENAGDVAFVKDVTV
LQNTDGNNNDAWAKDLKLADFALLCLGGKRKPVTEARSCHLAWAPNHAVVSRWDKVER
LKQVLLHQOARGGRNASDCPDKFCLTQGSTKNLLFNDNTECLARLHGKTTYEKYLGPQ
YVAGITNLKKCSTSPLLEACEFLRK*
30122 c 32403 g 39349 t
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127884...128068.130006...130073,132023...132154,
133863...134018,135022...135075,135890...135980,
137445...137599,138436...138610,139077...>139255))
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CSAVEVIGVLDNLIVVLILVKKGLKRVENIYLLLAVSNLCELITLEFWAHAGGDPM
CKILIGLYFVGLYSEIFHCLLTVQRYLVFLHKGNEFSAFRRVPGGIITSVLAWVFAL
LATLDEYVVYKPOMEDQKYKCAFSRTDFLDADETFWKHFLITLKNNISUVLDLEIFTFF
LYVQMRKTLREREQRYSLFKLVFAIMVVFLLMMAPYNIAFFLSTFKEHFSLSDCKSSY
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QAMQVTETLGMTHCCINPIIYAFVGEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="confirmed by similarity to lactoferrin protein, encoded by GenBank Accession Number M73700, gi 186818"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="confirmed by similarity to lactoferrin mRNA,
accession number M73700"
/product="lactoferrin"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Identified as a gene by Grail Version 1.3c.
Translated sequence exhibits 42% sequence identity to CCR5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Putative mRNA identified by homology to CCR5 mRNA.
/product="ccr6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASSVYTRSTGEQEISVGL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="lactoferrin"
/protein_id="AAB57795.1"
/db_xref="GI:2104522"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NLDKSVHITKLIATTHCCINPLLYAFLDGTFSKYLCRCFHLRSNTPLQPRGQSAQGTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /evidence=not_experimental
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)6642. .97676
                                                                                                                                                                                                                                                                                                                                                                                                                                         translation="DLSDEAERDEYELLCPDNTRKPVDKFKDCHLARVPSHAVVARSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'gene-"lactoferrin"
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                                                                                                                                                                                                            8.98;
                                                                                                                                                                           0;
                                                                                                                                                                                          Score 19; DB 11; Length 143068; Pred. No. 5.2;
DNA
10 clone 15022,
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SEQUENCING IN PROGRESS
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VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
                                                                                                        BASE COUNT
ORIGIN
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Source
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                                  Query Match
Best Local S
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
                    1 Similarity
19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            McCombie, W.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC018744.2 GI:7:
HTG; HTGS_PHASE1
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AC018744
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     McCombie, W.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      I 11724, USA

Mar 7, 2000 this sequence version replaced g1:6730690.

MOTE: This is a 'working draft' sequence. It currently consists of 16 contigs. The true order of the pieces is not known and their order in this sequence record is is not known and their order in this sequence as
                                                                                                                        62170
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                                                                                                                      /db_xref="taxon:4530"
/chromosome="10"
/clone="15022"
a 45887 c 47331 g 60
                                                                                                                                                                                            organism-"Oryza sativa"
                                                                                                                                                                                                                                  Location,
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1 (bases 1 to 2698)

Lee,F.J., Lin,L.W. and Smith,J.A.

Molecular cloning and sequencing of a cDNA encoding alpha-acetyltransferase from Saccharomyces cerevisia alpha-acetyltransferase from Saccharomyces (2018)

J. Biol. Chem. 264 (21), 12339-12343 (1989)
                                                                                18; Conserv
                                                                                                                                                                                        Chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Draft entry and computer-readable sequence [1] kindly submitted by F.-J.Lee, 10-APR-1989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae (strain TD71.8) (clone: pBN9) cDNA to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-acetyltransferase.
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FGTTSGLFGSMAIVLLHATRNDTPFDPILKKVVTKSLEKEYSENFPLNEISNNSFDWL
NFYQEKFGKNDINGLLFLYRYRDDVPIGSSNLKEMIISSLSPLEPHSQNEILQYYL"
                                                                                                                                                                                                                                                                                            RLYLDRKKKLDDLASLKKEVESDKSEQIANDIKENQWLVRKYKGLALKRFNAIPKFYK
QFEDDQLDFHSYCMRKGTPRAYLEMLEWGKALYTKPMYVRAMKEASKLYFQMHDDRLK
RKSDSLDENSDEIQNNGQNSSSQKKKAKKEAAAMNKKKETEAKSVAAYPSDQDNDVFG
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PQLERGYPATFSNYKPLYQRKSKYSPLLEKIYLDDYLSGJOPTQDFIPTHYNYYLSQ
HFLFLKDFFKAQEYIDAALDHTPTLYBEYILKARILKHLGLMDTAAGILEGGRQLDLO
DRFINCKTYKYFLRANNIDKAVEVASLFTKNDDSVNGIKDLHLVEASWFIVEQAEAYY
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NTKEYKESIKWFTAALNNGSTNKQIYRDLATLGSQIGDFKNALYGRKKWEAAFIGYRA
NWTSLAVAQDYNGERQOAINTLSGFEKLAEGKISDSEKYEHSECLMYKNDIJMYKAASD
NQDKLQNYLKHLNDIEPCYFDKFGLLERKATIYMKLGQLKDASIYYRTILIKRNPDNFK
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/protein_id="AAA88728.1"
/db_xref="GI:172028"
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/strain="TD71.8"
/db_xref="taxon:4932"
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'db_xref="SGD:S0002198"
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1 (bases 1 to 2699)
Smith, J.A. and Lee, F-J.S.
Isolation, purification, characterizat:
Of N alpha-acetyltransferase
Patent: Ep 0334004-A1 1 27-SEP-1989;
Location/Qualifiers
ce 1..2699
baker's yeast.
Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.
1 (bases 1 to 3347)
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
109397
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Yeast NAT 1 gene for N-terminal acetyltransferase.
X15135
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l Similarity 100.0%;
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                                                      acetyltransferase; NAT 1
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1 (bases 1 to 2724)

Smith,J.A. and Lee,F-J.S.

Patent: WO 8907138-A 5 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                        Paulin, L., S
Unpublished
                                                                                     Saccharomyces cerevisiae

Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.

1 (bases 1 to 3530)
                                                                                                                                                                                                                                            SCYDL040C 3530 bp
S.cerevisiae chromosome
Z74088 Z71256
Z74088.1 GI:1431024
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ilarity 100.0%;
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/db_xref="taxon:4932"
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                                                                      Saren, A.M. and Laamanen, P
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S.cerevisiae
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Z71781.1 GI:
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          Direct Submission
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                                                    (bases 1 to 36687)
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Submitted (09-UUL-1996) Data collected by MIPS on behalf of the European yeast chromosome IV sequencing project. MIPS at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a D-82152 Martinsried, FRG; E-mail: Mewes@mips.embnet.org
Saren,A.M., Laamanen,P., Lejarcegui,J.B. and Paulin,L. The sequence of a 36.7 kb segment on the left arm of chromosome IV from Saccharomyces cerevisiae reveals 20 non-overlapping open reading frames (ORFs) including SIT4, FAD1, NAM1, RNA11, SIR2, NAT1, PRP9, ACT2 and MPS1 and 11 new ORFs
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l similarity 100.0%;
18; Conservative
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                                                                                                                                                                                                                                                  Saccharomycetaceae; Saccharomyces.

1 (bases 1 to 36687)
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complement(419. .2983)
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gene		CDS	gene		gene CDS	GBS	JOURNAL FEATURES Source
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CDS	CDS gene			gene CDS		gene CDS	CDS
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SOURCE
ORGANISM
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ACCESSION
                                                            COMMENT
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S.pombe chromosome
AL034563
                                                                                     sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 15A, E-mail: barrell@sanger.ac.uk and Biotechnologische und molekularbiologische Forschung, Angelhofweg 39, D-69259 Wilhelmsfeld, Germany
                                                                                                                                                                                                                                                                                       Schlzosaccharomyces pombe
Eukaryota; Fung1; Ascomycota; Schlzosaccharomycetales;
Schlzosaccharomycetaceae; Schlzosaccharomyces.
1 (bases 1 to 43325)
                                                                                                                                                                                            Submitted (18-DEC-1998) European Schizosaccharomyces genome
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Details of yeast sequencing at the Sanger Centre the World Wide Web.
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DMOSOME II COSM1d c660.
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The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.

IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.

Cosmid c660 is overlapped at the 3' end by cosmid 1198 (contained in EMBL entry SP33010 accession number U33010).
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During 1995 to 1996 about 66% of S. pombe Chromosome 1 was
sequenced by the Sanger Centre. The sequencing of the S. pombe
genome is now being continued with funding from The European
Commission. Fourteen European sequencing laboratories, including
the Sanger Centre, are participating in the project.
Protein coding regions (CDS) have been predicted with the help of
computer analysis using the Genefinder program in PomBase (an ACEDB
database) with additional predictions for the branch-acceptor sites
supplied by the program Sp3splice. CAUTION: It is possible that for
any individual CDS we may have underestimated or overestimated the
number of introns/exons or we may not have chosen the correct
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CDS are numbered using the following system eg SPBC25H2.0lc. SP pombe), B (chromosome 2), c25H2 (cosmid name), .01 (first CDS),
                                                                                                                                /note-"ctaatattttaatttaag, splice branch complement(132. 137)
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/note-"gtaagt, splice donor sequence"
complement(join(383. 464,506. 537))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="SPBC660.01c, SIMILARITY:Schizosaccharomyces pombe,
CAB52717, putative myb-like dna-binding protein., (496
aa), fasta_scores: opt: 478, E():4.7e-23, (30.6% identity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(1. .1482)
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NIVKEANGRWTRD"
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11.1"
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'note="ttaacgtttag, splice branch and acceptor"

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acceptor"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(3930. .4184,4288. .4431,4491. .5015))
/gene="SPBC660.03c"
/note="SPBC660.03c"
/note="SPBC660.03c, len:307, SIMILARITY:Saccharomyces
cerev isiae, YGR005C, T2FB_YEAST, transcription initiation
factor if, beta subunit, (400 aa), fasta scores: opt:
461, E():2. 9e-32, (31.0% identity in 368 aa);
SPBC660.03c, len:307, SIMILARITY:Saccharomyces cerevisiae,
T2FB_YEAST, transcription initiation factor iif, beta
subunit, (400 aa), fasta scores: opt: 461, E():1.4e-22,
(31.0% identity in 368 aa)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="SPBC660.02"
/note="ctaacgacagcag, splice branch and acceptor"
3258. .3353
                                                                                                                                                                                                                VKQPEVYLKEVLDSIAILNKRGPYALKYSLKPEYKGTMDAASVELRNQQASQSESSSI
DHTGKNTSPDNPGTNAEEDEDDDGVEMIDVV"
                                                                                                                                                                                                                                                                              WNSIPEDDAANLGCVRVKNDEIQLLLQNSPENADVPKIYNLRVMNKFVRNSYVFRESE
TSSSMKSTALVGTVAHECNVSPVINDDYRRVMQKRALAASAPKRKVQMIDDRGGSLLA
PGTLGSRSRSTTSFIRNVKPRTGEGLKNSRIPRNELLDILFKCFEDYEYWTLKGLREY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DYRSSRPLHKFEEHTAAVKAIGWSPHQRGILASGGGTIDRCLTIHNTLTGRLQNKLDT
GSQVCNMAWSKTSNEIVTTHGFAKNQVSLWKYPSLKNIANLTAHTNRVLYLSMSPDGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HDFGATNHYTSYLWTGKGTQLAVGTDSGVIYIWDIESTKSVRSLKGHSERVAALAWND
NTLTSGGKDEVILHHDLRAPGCCAEMMKVHEQEICGLQWDRSLGQLASGGNDNNLFVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="Sptrembl:094423"
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fmellsmelfgsqsassraffygedkrriekkkldtpdrksyslspispqsqdmlrqp
qkpkrafpktpykildapylkndfylnlldmgqsnvlavglassiylmsaasgkvvql
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               join(2618. .2738,2785. .3929)

join(2618. .2738,2785. .3929)

gene-"SpBc660.02"

/note-"SpBc660.02, len:421, SIMILARITY:Schizosaccharomyces
pombe, O13286, srwl., (556 aa), fasta scores: opt: 1364,

E():0, (50.6% identity in 385 aa)"
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/db_xref="SPTREMBL:994424"
/translation="MSEEKPTVRTEEDDRYEDDAGDLDLGQIGSRVWLVKIPKFLMDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Match to PF00400 WD40, Score 20.22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIVTGAGDETLRFWKLFNKKPKEESTLIR"
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/gene="SPBC660.03c"
/note="gtatgt, splice donor sequence"
                                                                                                            /note="ctaatgaattcatattag,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Match to PF00400 WD40,
Score 31.68"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Match to PF00400 WD40,
Score 22.93"
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2618. .3929
                                                                                                                                            'gene-"SPBC660.03c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'product="transcription initiation factor iif, beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene-"SPBC660.02"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'codon_start=1
'label=SPBC660.03c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'gene="SPBC660.02"
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'protein_id="CAA22522.1"
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                                                                                                                                                                                    .4202)
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                                                                                                            splice
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                                                                                                               branch
                                                                                                        and acceptor"
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AUTHORS
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SOURCE
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AC022747/c
       COMMENT
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Best Local S
Matches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
TITLE
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                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
les 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                        Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dewarlano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McKernan, McKernan
Submitted (06-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker:
                                                                                                                                                                         McPheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylot, J., Nornam, C.H., O'Connor, T., O'Donnell, P., Ollvar, T.M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Birren, B., Linton, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens chromosome Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 83536)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 4, clone RP11-131K9
                                                                                                            Zimmer, A. and Zody, M. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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/gene="SPBC660.04c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SKHEVEEYINFIK"
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GELSLLLNSLQFSFKFIANTIRKAELVNLIGLSGIVNSTGDEQKKLDKICNDIFITAM
KSNGCCKLIVSEEEEDLIVVDSNGSYAVTCDFIDGSSNIDAGVSVGTIFGIYKLRPGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QGDISDVLRPGKEMVAAGYTMYGASAHLLLTTGHRVNGFTLDTDIGEFILTHRNMKMP
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/gene="SPBC660.04c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="gtatgt, splice donor sequence"
complement(6039 .7082)
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/protein_1d="CAA22524.1"
/db_xref="GI:4049503"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="SPBC660.03c"
'note="~--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 to 83536)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="SPBC660.04c, len:347; SPBC660.04c, len:347"
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/db_xref="taxon:9606"
/chromosome="11"
                                                                                                               clone="CMB9-21K9"
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Submitted (03-FEB-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Mar 21, 2000 this sequence version replaced gi:6862782.

------Genome Center

Center: Joint Genome Institute

Center Code: JGI

Web site: http://www.jgi.doe.gov

-------Summary Statistics

Consensus quality: 118702 bases at least Q40

Consensus quality: 13055 bases at least Q30

Consensus quality: 13055 bases at least Q30

Consensus quality: 133293 bases at least Q30

Estimated insert size: 149000; pulse field gel estimation Quality coverage: 3.58x in Q20 bases; pulse field gel estimation Quality coverage: 3.78x in Q20 bases; sum-of-contigs estimation
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Homo sapiens chromosome
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1 (bases 1 to 141107)

DOE Joint Genome Institute.

Sequencing of Human Chromosome 5

Unpublished
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HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 30 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                           be preserved.
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Joint Genome Institute.
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contig of 1383 bp in length
gap of unknown length
19355: contig of 1794 bp in length
contig of 1794 bp in length
21747: contig of 2965 bp in length
227513: contig of 2965 bp in length
gap of unknown length
27513: contig of 2801 bp in length
gap of unknown length
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/chromsome="5"
/clone="CTC-316M18"
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/note="L1 repeat: matches 5390. .5194 of consensus"
2854. .3352
/note="L1ME1 repeat: matches 60"
2971. .3352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3327. .3559 ----- matches 3/v. .1/v of consensus /note="MER20 repeat: matches 1. .218 of consensus" 3580. .3873
/note="match: multiple ESTs; match: R71060 H69028 R82016 R10102 R82280 R82281; match: R82066 H69792 H79486 AA506861 T78091; match: W03874 H74282 D85329" complement(join(27431 .27577,28562 .28744,31530 .31681,3638 .33782,36315 .36470,36919 .37022,37955 .38026,39019 .39135,41033 .41212,42726 .42936,43904 .44140,49624 .49798,53412 .56232,57414 .56282,58300 .59710,62919 .63133,63758 .63857,65675 .65862,68300 .68465,69764 .69985,72271 .72414,73672 .73884,85339 .85461,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1876. 2745
/note="L1MB5 repeat: matches 921. .1 of consensus" 2597. .2793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1410. .1587
/note="MLT1D repeat: matches 139.
1575. .1858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note
22748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13253. .13367
/note="MIR2 repeat: matches 4. .127 of consensus"
13398. .15749
/note="L1_repeat: matches 2577. .4940 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Alusq repeat: matches 303. .1 of consensus" 13253. .13367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7024. 7238
'note="AluY repeat: matches 84. .299 of consensus;
incomplete repeat"
                                                                                                                                                                                     /note="L1MA7 repeat: matches 1017. 27046. .>27579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="THE1C
12196. .12497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="MIR repeat: matches 89. .262 of consensus" complement(10749. .11106) /note="match: STS G05144" 11725. .12081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="AluSc repeat: matches 2.
10054. .10223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6468.
                                                                                                                                                                                                                                                                                                                                                                                                                                         <25068
                                                                                                                                                                                                                                                                     /note="MLT1F repeat: matches 18.
26055. .26264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16076. .16554
/note="L1 repeat: matches 4910. .5390 of consensus"
16409. .17294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="MIR2 repeat: matches 22. .145 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note-"L1MC2 repeat: matches 193.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="Alusc repeat: matches 1. .299 of consensus"
                                                                                                                                                                                                                                                                                                                                                                         note="MIR repeat: matches 49.
                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="L1MB5 repeat: matches 812.
<25068. .25543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          e="L1PA2 repeat: matches 1. .891 of consensus"
8. .19825
                                                                                                                                                                                                                                                                                                                                                                                                             e-"match: H61071 H69565"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e="L1PA6 repeat: matches 1. .890 of consensus"
2. .22827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   % "L1 repeat: matches 3338. .5390 of consensus"
3. .20571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -"L1MB4 repeat: matches 797.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .4060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "THEIC repeat: matches 371.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IME2 repeat: matches 570.
                                                                                                                                                                                                                                                repeat: matches 2971. .2759 of consensus"
                                                                                                                                                                                                                                                                                                                             repeat: matches 1. .178 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           matches 265.
                                                                                                                                                                                                                                                                                                                                                                           .131 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .295 of consensus"
                                                                                                                                                                                                                                                                                         .138 of consensus
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HFTGHSFIYGKRHEDTLTLFPMRGESVTVTMDNVGTWMLTSMNSPRSKKLRKERDV
KCIPDDEDSYEIFEDPESTVMATRKMIDRLEPEDEESDADIVDQNRLAAALGIRSFR
NSSLNQEEEEFNLTFALALENGTEFVSSNTDIIVGSNYSSPSNISKFTVNNLAEPOKAS
SHQQATTAGSPLRHLIGKNSVLNSSTAEHSSPYSEDPIEDPLQPDVTGIRLLSLGAGE
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VDIMRDIASGLIGLLLICKSRSLDRQGIQRAADIEQQAVFAVFDENKSWYLEDNINKF
CENPDEVKRDDPKFYESNIMSTINGYVPESITTLGFCFDDTVQWHFCSVGTQNEILTI
                                                                                                                                                                                                                                                                                         EKKSRSSWRLTSSEMKKSHEFHAINOMIYSLPGLKMYEQEWVRLHLLNIGGSQDIHVV
HFHGQTLLENGNKQHQLGVWPLLPGSFKTLEMKASKPGWWLLNTEVGENQRAGMQTPF
LIMDRDCRMPMGLSTGIISDSQIKASEFLGYWEPRLARLNNGGSYNAWSVEKLAAEFA
SKPWIQVDMQKEVIITGIQTQGAKHYLKSCYTTEFYVAYSSNQINWQIFKGNSTRNVM
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ISPDLSHTTLSLDFSQTNLSPELSQTNLSPALGOMPLSPDPSHTTLSLDLSQTNLSPE
LSQTNLSPDLSEMPLFADLSQIPLTPDLDQMTLSPDLGETDLSPNGGQMSLSPDLSQV
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THDDPPCLTHIYYSHENLIEDFNSGLIGPLLICKKGTLTEGGTQKTFDKQIVLLFAVF
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/protein_id="CAB16748.1"
/db_xref="GI:2769647"
                                                                                                                                                                                                     GK I ENKQITASSFKKSWWGDYWEPFRARLNAQGRVNAWQAKANNNKQWLEIDLLKIKF
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SPTLNDTFLSKEFNPLVIVGLSKDGTDYIEIIPKEEVQSSEDDYAEIDYVPYDDPYKT
DVRTNINSSRDPDNIAAWYLRSNNGNRRNYYIAAEEISWDYSEFVQRETDIEDSDDIP
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RSSSPELSEMLEYDRSHKSFPTDISQMSPSSEHEVWQTVISPDLSQVTLSPELSQTNL
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AWAYYSAVNPEKDIHSGLIGPLLICQKGILHKDSNMPMDMREFVLLFMTFDEKKSWYY
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!RPEPTNSSLNLSVTSFKKIVYREYEPYFKKEKPQSTISGLLGPTLYAEVGDIIKVHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="SPTREMBL:043737"
.140
0f
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/note="L1 38333. .30451 note-"AluJo repeat: matches 1. incomplete repeat" 40215. .40272 31903. .31988 /note="MIR repeat: matches 104. .17 of consensus" 29041. .29084 /note="MIR2 r 27629...27788
/note="AluJo repeat: matches incomplete repeat" 28002...28176 /note="MADE1 repeat: matches 1. 43274. .43327 /note="Alusc repeat: matches 299. .1 of consensus" 35051. .35542 /note="MIR repeat: matches 75. .259 of consensus" note="MIR2 repeat: note="MIR repeat: matches 40. .235 of consensus" .38451 l repeat: matches 3215. .3729 of consensus" 18808 matches 146. .93 of consensus" 302. .53 of consensus .134 of .146 of consensus" consensus; consensus;

repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region

repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region

/note="L1MA8 repeat: matches 1038. .944 of consensus" 44951. .46774

/note="11 repeat: matches 3613. 46627. .46980 /note="11MA7 repeat: matches 2.

LIMA7 repeat: matches 2.

.364 of consensus"

.5390 of consensus"

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ORIGIN
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KEYWORDS
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TITLE
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                                                                                Matches
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                62087
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                  AAAACATCTACTTTGAAA 62104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         consensus quality: 132291 bases at least Q40
Consensus quality: 133293 bases at least Q30
Consensus quality: 133633 bases at least Q20
Estimated insert size: 133733 bases field gel estimation
Estimated insert size: 233000; pulse field gel estimation
Quality coverage: 4.87x in Q20 bases; pulse field gel estimation
Quality coverage: 8.48x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Apr 5, 2000 this sequence version replaced g1:7212886.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Joint Genome Institute Center Code: JGI
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DOE Joint Genome Institute.
Sequencing of Human Chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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DOE Joint Genome Institute.
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HTG: HTGS_PHASE1; HTGS_DRAFT
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                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence, It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                           43496
                                                                                Conservative
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                                                                                                                                                                     /chromosome="5"
/clone="CTD-2199L14"
25289 c 24707 g 40291 t
                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                      3 133783: contig of 124121 bp in length
Location/Qualifiers
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                                                                        8.4%; occ
100.0%; Pr
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100.0%;
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Primates;
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Pred. No.
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5 clone CTD-2199L14, WORKING DRAFT
                                                                                Mismatches
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                                                                                         DB 72;
19;
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                                                                                                           Length 133783;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9924)
On Feb 19, 2000 this sequence version replaced gi:6997652.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujlyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Direct Submission
Submitted (03-DEC-1999) to the DDBJ/EMBL/GenBank databases.
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1 (Dases 1 to 139740)

Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo sapiens 139,740 genomic DNA of 11922

Published Only in DataBase (1999) In press

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be preserved.
Smit, A.F.A. & Green, P. (1996–1997)
http://ftp.genome.washirgton.edu/RM/RepeatMasker.html
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Gaps

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Indels

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1600 others

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Cambridgeshire, CB10 1SA, UK. E-mail enquires:

Cambridgeshire, CB10 1SA, UK. E-mail enquires:

Cambridgeshire, CB10 1SA, UK. E-mail enquires:

humquery@sanger.ac.uk/GPChri/) Sanger Centre,

n Jan 13, 1998 this sequence version replaced gi:2578147.

IMPORTANT: This sequence ts not the entire insert of clone 86F14.

It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variations annotated may not be found in the sequence submission corresponding to the overlapping clone as we submit sequences with small overlap, as described above.

This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre chromosome 1 http://www.sanger.ac.uk/HGP/Chri/ This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequence map criteria as follows. An attempt is made to resolve all sequence map criteria as follows. An attempt is made to resolve all sequence has sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                    HS86F14 106571 bp DNA PRI 23-NOV-1999
Human DNA sequence from PAC 86F14 on chromosome 1q23-1q24. Contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The true right end of clone 206D15 is at 104.

The true right end of clone 86F14 is at 106571.

B6F14 is from the library RPCII constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong.

For further details see http://bacpac.med.buffalo.edu/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 106571)
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/note="AluSx repeat: matches 1. .302 of consensus"
1270. .1360
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                                                                                                                                                                      DB 40; Length 102995; 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (13-JAN-1998) Chromosome 1 Project Group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lq23-1q24; blood coagulation factor; factor V.
                  /clone="RPI-278E11"
/clone_lib="RPCI-1"
22682 c 22914 g 27418 t
                                                                                                                                                                                                  100.0%; Pred. No. 19;
tive 0; Mismatches
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/db_xref="taxon:9606"
                                                                                                                                                                        8.4%; Score 18;
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/clone="RP1-86F14"
                                                                                                                                                                                                                                                                                                     Db 77128 CTTTGAAACATCTACTGG 77145
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Best Local Similarity 100.
Matches 18; Conservative
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                                                                      BASE COUNT
ORIGIN
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HS86F14/c
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JOURNAL
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KEYWORDS
SOURCE
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IMPORTANT This sequence version replaced g1:7320935.

IMPORTANT This sequence work on the sequence is in progress and the release of this data is based on the understanding that the sequence may obe coitaminated with foreign sequence from E.coli, yeast, vector, phage etc. Order of segments is not known; 800 n's separate segments. Contig_ID: 00773 Length: 7736bp

Contig_ID: 00773 Length: 7502bp

* NOTE: This is a "working draft' sequence. It currently

* Contig_ID: 00923 Length: 76087bp

* Angle ID: 00924 Length: 76087bp

* Angle ID: 0044 Sequence record is

* is not known and their order in this sequence record is

* this record will be updated with the finished sequence

* As soon as it is available and the accession number will

* be preserved.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae, Homo.
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Location/Qualifiers
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gap of unknown length
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unknown length
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unknown length
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0; Mismatches
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Homo sapiens chromosome 6 clone F
PROGEESS ***, 3 unordered pieces.
AL136089 GI:7530184
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/db_xref="taxon:9606"
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human,

ORGANISM

KEYWORDS SOURCE

AUTHORS TITLE REFERENCE

JOURNAL

COMMENT

DEFINITION

AL136089

RESULT

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ACCESSION VERSION

source

FEATURES

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